

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 08:48:29 ; Search time 12.59 Seconds
(without alignments)
321.731 Million cell updates/sec

Title: US-09-828-000-3
Perfect score: 180
Sequence: 1 EPAVYFKQFLDGDGWTSRW.....PDNTYEVKIDNSQVSGSLE 180

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 212252 seqs, 22503292 residues

Word size : 18

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description

No matches found

Search completed: January 14, 2002, 08:50:22
Job time: 113 sec

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OM protein - protein search, using sw model

Run on: January 14, 2002, 08:49:15 ; Search time 14.43 Seconds
(without alignments)
950.202 Million cell updates/sec

Title: US-09-828-000-3
Perfect score: 180
Sequence: 1 EPAYVFEQFLDGDGWTSRW.....PDNTYEVKIDNSQVESGSL 180

Scoring table:
OLIGO 60.0 , Gapext 60.0
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 18

Total number of hits satisfying chosen parameters: 12

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	180	100.0	417	1 A37047	calreticulin precu
2	77	42.8	416	1 S05763	calreticulin precu
3	77	42.8	416	2 JH0819	calreticulin precu
4	77	42.8	418	1 A34154	calreticulin precu
5	62	34.4	400	2 S43376	calreticulin, brai
6	62	34.4	421	2 S36799	calreticulin precu
7	27	15.0	405	1 JH0795	calreticulin precu
8	22	12.2	384	2 S29130	calreticulin (clon
9	22	12.2	411	2 S29129	calreticulin precu
10	20	11.1	419	2 S71343	calreticulin precu
11	19	10.6	336	2 A32507	41K larval antigen
12	19	10.6	406	2 A56637	calreticulin homol

ALIGNMENTS

RESULT 1
A37047
calreticulin precursor - human
N:Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K integrin-binding prote
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Feb-2000
C:Accession: A42330; A37047; A46452; A28812; PH1525; A40346; S11475; T45075
R:McCaulliffe, D.P.; Yang, Y.S.; Wilson, J.; Sontheimer, R.D.; Capra, J.D.
J. Biol. Chem. 267, 2557-2562, 1992
A:Title: The 5'-flanking region of the human calreticulin gene shares homology with the
A:Reference number: A42330; MUID:92129342
A:Accession: A42330

A:Molecule type: DNA
A:Residues: 1-417 <MC2>
A:Note: sequence extracted from NCBI backbone (NCBIN:78537, NCBIP:78536)
R:McCaulliffe, D.P.; Lux, F.A.; Lieu, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachin
J. Clin. Invest. 85, 1379-1391, 1990
A:Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/
A:Reference number: A37047; MUID:90237213
A:Accession: A37047
A:Molecule type: mRNA
A:Residues: 1-417 <MC2>
A:Cross-references: GB:M32294; NID:g337486; PIDN:AAA36582.1; PID:g337487
A:Note: the authors translated the codon GTA for residue 349 as Tyr
R:Kokach, L.A.; Haselby, J.A.; Meilof, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.
J. Immunol. 147, 3031-3039, 1991
A:Title: Characterization of the autoantigen calreticulin.
A:Reference number: A46452; MUID:92013129
A:Accession: A46452
A:Molecule type: mRNA
A:Residues: 1-417 <ROK>
A:Cross-references: GB:M84739; NID:gl79881; PIDN:AAA51916.1; PID:gl79882
A:Note: sequence extracted from NCBI backbone (NCBIN:60749, NCBIP:60750)
R:Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sontheimer, R.D.
J. Clin. Invest. 82, 96-101, 1988
A:Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence
A:Reference number: A28812; MUID:88273610
A:Accession: A28812
A:Molecule type: protein
A:Residues: 18-41 <LIE>
A:Note: 18-Ala was also found
R:Dupuis, M.; Schaefer, E.; Krause, K.H.; Tschoep, J.
J. Exp. Med. 177, 1-7, 1993
A:Title: The calcium-binding protein calreticulin is a major constituent of lytic gra
A:Reference number: PH1525; MUID:93115648
A:Accession: PH1525
A:Molecule type: protein
A:Residues: 18-27 <DUP>
A:Experimental source: LAK cell
R:Roiani, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.
Biochemistry 30, 9859-9866, 1991
A:Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (c
A:Reference number: A40346; MUID:9202034
A:Accession: A40346
A:Molecule type: protein
A:Residues: 18-34,'R' <ROJ>
R:Krause, K.H.; Simmerman, H.K.B.; Jones, L.R.; Campbell, K.P.
Biochem. J. 270, 545-548, 1990
A:Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that corpu
A:Reference number: S11475; MUID:90380058
A:Accession: S11475
A:Molecule type: protein
A:Residues: 18-32 <KRA>
R:Lamerdin, J.; McGready, P.; Stilwagen, S.; Ramirez, M.; Carrano, A.
submitted to the EMBL data Library, November 1996
A:Description: Characterization by genomic sequence analysis of a gene-rich 111 kb re
A:Reference number: 222906
A:Accession: T45075
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-417 <LAM>
A:Cross-references: EMBL:AD000092; PIDN:AAB51176.1
A:Experimental source: cell line 5HL2-B; fibroblast
C:Comment: Autoantibodies specific for this protein are found in Sjogren's syndrome a
C:Genetics:
A:Gene: GDB:CALR
A:Cross-references: GDB:125179; OMIM:109091
A:Map position: 19p13.3-19p13.2
A:Introns: 31/1; 65/1; 133/1; 164/3; 234/3; 272/3; 320/3; 351/3
A:Note: CRTG
C:Superfamily: calreticulin
C:Keywords: calcium binding; integrin binding
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-417/Product: calreticulin #status predicted <MAT>
F;414-417/Region: endoplasmic reticulum retention signal

A;Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage
A;Reference number: S13045; MUID:91054414
A;Accession: S13045
A;Molecule type: protein
A;Residues: 18-29 <PRE>
C;Superfamily: calreticulin
C;Keywords: calcium binding; glycoprotein
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-416/Product: calreticulin #status experimental <MAT>
F;204-212/Region: nuclear location signal
F;413-416/Region: endoplasmic reticulum retention signal
F;344/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 42.8%; Score 77; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 5.2e-74;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 DMHGDSEYNMFPGDGGCTKKVHVIFNYKGNVLINKDIRCKDDFFTHLYTLIVRPD 163
|||||
Db 121 DMHGDSEYNMFPGDGGCTKKVHVIFNYKGNVLINKDIRCKDDFFTHLYTLIVRPD 180
|||||

QY 164 TYEVKIDNSQVESGSLE 180
|||||
Db 181 TYEVKIDNSQVESGSLE 197
|||||

RESULT 4
A34154
calreticulin precursor, skeletal muscle - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
A;Accession: A34154; S13047
R;Fliegel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M.
J. Biol. Chem. 264, 21522-21528, 1989
A;Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin) c
A;Reference number: A34154; MUID:90094320
A;Status: preliminary
A;Accession: A34154
A;Molecule type: mRNA
A;Residues: 1-418 <FLI>
A;Cross-references: GB:J05138; NID:g164858; PIDN:AAA31188.1; PID:g164859
R;Treves, S.; de Mattel, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld
Biochem. J. 271, 473-480, 1990
A;Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage
A;Reference number: S13045; MUID:91054414
A;Accession: S13047
A;Molecule type: protein
A;Residues: 19-32 <PRE>
C;Superfamily: calreticulin
C;Keywords: skeletal muscle
F;1-17/Domain: signal sequence #status predicted <SIG>
F;415-418/Region: endoplasmic reticulum retention signal

Query Match 42.8%; Score 77; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 5.2e-74;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 DMHGDSEYNMFPGDGGCTKKVHVIFNYKGNVLINKDIRCKDDFFTHLYTLIVRPD 163
|||||
Db 121 DMHGDSEYNMFPGDGGCTKKVHVIFNYKGNVLINKDIRCKDDFFTHLYTLIVRPD 180
|||||

QY 164 TYEVKIDNSQVESGSLE 180
|||||
Db 181 TYEVKIDNSQVESGSLE 197
|||||

RESULT 5
S43376
calreticulin, brain isoform 1 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Oct-1994 #sequence_revision 23-Mar-1995 #text_change 07-May-1999

C;Accession: S43376; S36801
R;Matsuoka, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isobe, T.
Biochem. J. 298, 435-442, 1994
A;Title: Covalent structure of bovine brain calreticulin.
A;Reference number: S43376; MUID:94183174
A;Accession: S43376
A;Molecule type: protein
A;Residues: 1-400 <MAT>
A;Experimental source: brain
R;Liu, N.; Fine, R.E.; Johnson, R.J.
Biochim. Biophys. Acta 1202, 70-76, 1993
A;Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticuli
A;Reference number: S36799; MUID:93385184
A;Accession: S36801
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 45-63, 'E', 65-83 <LIU>
A;Experimental source: brain, clone 8.1
C;Superfamily: calreticulin
C;Keywords: calcium binding; glycoprotein
F;397-400/Region: endoplasmic reticulum retention signal
F;120-146/Disulfide bonds: #status experimental
F;162/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 34.4%; Score 62; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 5e-58;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 LDQTDHMGDSEYNMFPGDGGCTKKVHVIFNYKGNVLINKDIRCKDDFFTHLYTLIV 159
|||||
Db 100 LDQTDHMGDSEYNMFPGDGGCTKKVHVIFNYKGNVLINKDIRCKDDFFTHLYTLIV 159
|||||

QY 160 RP 161
||
Db 160 RP 161
||

RESULT 6
S36799
calreticulin precursor, brain isoform 2 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Dec-1993 #sequence_revision 23-Mar-1995 #text_change 13-Aug-1999
A;Accession: S36799; S36800
R;Liu, N.; Fine, R.E.; Johnson, R.J.
Biochim. Biophys. Acta 1202, 70-76, 1993
A;Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticuli
A;Reference number: S36799; MUID:93385184
A;Accession: S36799
A;Molecule type: mRNA
A;Residues: 1-421 <LIU>
A;Cross-references: GB:L13462; NID:g348693; PIDN:AAC37307.1; PID:g348694
A;Experimental source: brain, clone 9.4
A;Accession: S36800
A;Molecule type: protein
A;Residues: 35-45 <LI2>
C;Superfamily: calreticulin
C;Keywords: calcium binding; glycoprotein
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-421/Product: calreticulin, brain isoform 2 #status predicted <MAT>
F;418-421/Region: endoplasmic reticulum retention signal
F;141-167/Disulfide bonds: #status predicted
F;183/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 34.4%; Score 62; DB 2; Length 421;
Best Local Similarity 100.0%; Pred. No. 5.2e-58;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 LDQTDHMGDSEYNMFPGDGGCTKKVHVIFNYKGNVLINKDIRCKDDFFTHLYTLIV 159
|||||
Db 121 LDQTDHMGDSEYNMFPGDGGCTKKVHVIFNYKGNVLINKDIRCKDDFFTHLYTLIV 180
|||||

QY 160 RP 161
||
Db 181 RP 182

RESULT 7
calreticulin precursor - California sea hare
N:Alternate names: protein 407
C:Species: Aplysia californica (California sea hare)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0795; B31409; F60977
R:Kennedy, T.E.; Kuhl, D.; Barzilal, A.; Sweatt, J.D.; Kandel, E.R.
Neuron 9, 1013-1024, 1992
A:Title: Long-term sensitization training in aplysia leads to an increase in calreticulin
in Aplysia.
A:Reference number: JH0795; MUID:9308937
A:Accession: JH0795
A:Molecule type: mRNA
A:Residues: 1-405 <KEN>
A:Cross-references: GB:S51239; NID:g262053; PIDN:AAB24569.1; PID:g262054
A:Experimental source: abdominal ganglion and antral nervous system
R:Kennedy, T.E.; Gawinowicz, M.A.; Barzilal, A.; Kandel, E.R.; Sweatt, J.D.
Proc. Natl. Acad. Sci. U.S.A. 85, 7008-7012, 1988
A:Title: Sequencing of proteins from two-dimensional gels by using in situ digestion and
tion in Aplysia.
A:Reference number: A94207; MUID:88320566
A:Accession: B31409
A:Molecule type: protein
A:Residues: 'X', 17-28, 'X', 30-31 <KE2>
R:Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilal, A.; Karl, K.
Electrophoresis 10, 152-157, 1989
A:Title: Development of a database of amino acid sequences for proteins identified and
A:Reference number: A60977; MUID:89276264
A:Accession: F60977
A:Molecule type: protein
A:Residues: 'X', 17-28, 'X', 30-31 <SWE>
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-405/Product: calreticulin #status experimental <MAT>
F:402-405/Region: endoplasmic reticulum retention signal

Query Match 15.0%; Score 27; DB 1; Length 405;
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 YNMFQDPCGPGTKVHVFNKGN 137
|||||
Db 124 YNMFQDPCGPGTKVHVFNKGN 150
|||||

RESULT 8
calreticulin (clone 8) - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: S29130; T01068
R:Traves, S.; Zorzato, F.; Pozzan, T.
Biochem. J. 287, 579-581, 1992
A:Title: Identification of calreticulin isoforms in the central nervous system.
A:Reference number: S29129; MUID:93074997
A:Accession: S29130
A:Molecule type: mRNA
A:Residues: 1-384 <TR>
A:Cross-references: EMBL:X67598
A:Accession: T01068
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-339, 'XTGR' <TR>
A:Cross-references: EMBL:X67598; NID:g64610; PIDN:CAA47867.1; PID:g64611
A:Experimental source: CNS
C:Superfamily: calreticulin

C:Keywords: glycoprotein
F:381-384/Region: endoplasmic reticulum retention signal
F:316/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.2%; Score 22; DB 2; Length 384;
Best Local Similarity 100.0%; Pred. No. 2.2e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 FTHLYTLIVRPDNTYEVKIDNS 172
|||||
Db 140 FTHLYTLIVRPDNTYEVKIDNS 161
|||||

RESULT 9
S29129
calreticulin precursor (clone 3) - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: S29129
R:Traves, S.; Zorzato, F.; Pozzan, T.
Biochem. J. 287, 579-581, 1992
A:Title: Identification of calreticulin isoforms in the central nervous system.
A:Reference number: S29129; MUID:93074997
A:Accession: S29129
A:Molecule type: mRNA
A:Residues: 1-411 <TR>
A:Cross-references: EMBL:X67597; NID:g64608; PIDN:CAA47866.1; PID:g64609
C:Superfamily: calreticulin
C:Keywords: glycoprotein
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F:13-411/Product: calreticulin #status predicted <MAT>
F:408-411/Region: endoplasmic reticulum retention signal
F:339/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.2%; Score 22; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 2.4e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 FTHLYTLIVRPDNTYEVKIDNS 172
|||||
Db 163 FTHLYTLIVRPDNTYEVKIDNS 184
|||||

RESULT 10
S71343
calreticulin precursor - Korean frog
C:Species: Rana rugosa (Korean frog)
C:Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 20-Jun-2000
C:Accession: S71343
R:Yamamoto, S.; Nakamura, M.
FEBS Lett. 387, 27-32, 1996
A:Title: Calnexin: its molecular cloning and expression in the liver of the frog, Ran
A:Reference number: S71342; MUID:96234004
A:Accession: S71343
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-419 <YAM>
A:Cross-references: EMBL:D78589; NID:g1514956; PIDN:BAA11425.1; PID:g1514957
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-419/Product: calreticulin #status predicted <MAT>
F:205-213/Region: nuclear location signal
F:415-418/Region: endoplasmic reticulum retention signal

Query Match 11.1%; Score 20; DB 2; Length 419;
Best Local Similarity 100.0%; Pred. No. 3.3e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 HLYTLIVRPDNTYEVKIDNS 172

Search completed: January 14, 2002, 08:51:14
Job time: 119 sec

```
Db 171 HLYTLIVRPNTYEVKIDNS 190
|||||
RESULT 11
A32507
41K larval antigen - nematode (Onchocerca volvulus) (fragment)
C:Species: Onchocerca volvulus
C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 12-Apr-1995
C:Accession: A32507; A28813
R:Unnasch, T.R.; Gallin, M.Y.; Soboslay, P.T.; Erttmann, K.D.; Greene, B.M.
J. Clin. Invest. 82, 262-269, 1988
A:Title: Isolation and characterization of expression cDNA clones encoding antigens of O
A:Reference number: A92769; MUID:88273584
A:Accession: A32507
A:Molecule type: mRNA
A:Residues: 1-336 <UNN>
C:Superfamily: calreticulin

Query Match 10.6%; Score 19; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 3.2e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 IMFGPDICGPGTKKVVHVF 131
|||||
Db 76 IMFGPDICGPGTKKVVHVF 94

RESULT 12
A56637
calreticulin homolog precursor - fruit fly (Drosophila melanogaster)
N:Alternate names: Ro/SS-A autoantigen/calreticulin homolog
C:Species: Drosophila melanogaster
C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 13-Aug-1999
C:Accession: A56637; A37158
R:Smith, M.J.
DNA Seq. 3, 247-250, 1992
A:Title: Nucleotide sequence of a Drosophila melanogaster gene encoding a calreticulin h
A:Reference number: A56637; MUID:93208374
A:Accession: A56637
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-406 <SMI>
A:Cross-references: GB:X64461; NID:g7685; PIDN:CAA45791.1; PID:g7686
A>Note: sequence extracted from NCBI backbone (NCBIN:128274, NCBIIP:128275)
R:McCaulliffe, D.P.; Zappi, E.; Lieu, T.S.; Michalak, M.; Sontheimer, R.D.; Capra, J.D.
J. Clin. Invest. 86, 332-335, 1990
A:Title: A human Ro/SS-A autoantigen is the homologue of calreticulin and is highly hom
A:Reference number: A37158; MUID:90307981
A:Accession: A37158
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: DNA
A:Residues: 91-105, 'A', 107, 109-124; 182-183, 'L', 185-220 <MCC>
C:Genetics:
A:Gene: FlyBase:Crc
A:Cross-references: FlyBase:FBgn0005585
A:Introns: 65/1; 222/3
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F;1-17/Domain: signal sequence #status predicted <SIG>
F;403-406/Region: endoplasmic reticulum retention signal

Query Match 10.6%; Score 19; DB 2; Length 406;
Best Local Similarity 100.0%; Pred. No. 3.7e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 IMFGPDICGPGTKKVVHVF 131
|||||
Db 130 IMFGPDICGPGTKKVVHVF 148
```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 08:49:34 ; Search time 11.77 Seconds
(without alignments)
560.720 Million cell updates/sec

Title: US-09-828-000-3
Perfect score: 180
Sequence: 1 EPAYVKEQFLDGDGWTSRM.....PDNTYEVKIDNSQVSGSLE 180
Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 100059 seqs, 36664827 residues
Word size : 18
Total number of hits satisfying chosen parameters: 9
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Listing first 45 summaries
Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	180	100.0	417	1	CRTC_HUMAN	P27797	homo sapien
2	77	42.8	416	1	CRTC_MOUSE	P14211	mus musculus
3	77	42.8	416	1	CRTC_RAT	P18418	rattus norv
4	77	42.8	418	1	CRTC_RABIT	P15253	oryctolagus
5	62	34.4	400	1	CRT1_BOVIN	P52193	bos taurus
6	62	34.4	421	1	CRT2_BOVIN	P42918	bos taurus
7	25	13.9	105	1	CRTC_PIG	P28491	sus scrofa
8	19	10.6	388	1	RALI_ONCVO	P11012	onchocerca
9	19	10.6	406	1	CRTC_DROME	P29413	drosophila

ALIGNMENTS

RESULT 1
CRTC_HUMAN
ID CRTC_HUMAN STANDARD; PRT; 417 AA.
AC P27797.
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (52 KDA
DE RIBONUCLEOPROTEIN AUTOANTIGEN RO/SS-A).
GN CALR OR CRTC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Plrimates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92013129; PubMed=1919005;
RA Rokeach L.A., Hazelby J.A., Mello J.F., Smeenk R.J., Unnasch T.R.,
RA Greene B.M., Hoch S.O.;

RT "Characterization of the autoantigen calreticulin.";
RL J. Immunol. 147:3031-3039(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90237213; PubMed=2332496;
RA McCaulliffe D.P., Lux F.A., Lieu T.S., Sanz I., Hanke J., Newkirk M.M.,
RA Bachinski L.L., Itoh Y., Siciliano M.J., Reichlin M., Sontheimer R.D.,
RA Capra J.D.;
RT "Molecular cloning, expression, and chromosome 19 localization of a
RT human Ro/SS-A autoantigen.";
RL J. Clin. Invest. 85:1379-1391(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92129342; PubMed=1733953;
RA McCaulliffe D.P., Yang Y.S., Willson J., Sontheimer R.D., Capra J.D.;
RT "The 5'-flanking region of the human calreticulin gene shares
RT homology with the human GRP78, GRP94, and protein disulfide isomerase
RT promoters.";
RL J. Biol. Chem. 267:2557-2562(1992).
RN [4]
RP SEQUENCE FROM N.A.
RA Lamerdin J., McCreedy P., Stillwagen S., Ramirez M., Carrano A.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 18-36.
RX MEDLINE=92002034; PubMed=1911778;
RA Rojiani M.V., Finlay B.B., Gray V., Dedhar S.;
RT "In vitro interaction of a polypeptide homologous to human Ro/SS-A
RT antigen (calreticulin) with a highly conserved amino acid sequence in
RT the cytoplasmic domain of integrin alpha subunits.";
RL Biochemistry 30:9859-9866(1991).
RN [6]
RP SEQUENCE OF 18-32.
RX MEDLINE=90380058; PubMed=2400400;
RA Krause K.H., Simmerman H.K.B., Jones L.R., Campbell K.P.;
RT "Sequence similarity of calreticulin with a Ca2(+)-binding protein
RT that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60
RT cells.";
RL Biochem. J. 270:545-548(1990).
RN [7]
RP SEQUENCE OF 18-28.
RC TISSUE=Liver;
RX MEDLINE=93162045; PubMed=1286669;
RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,
RA Appel R.D., Hughes G.J.;
RT "Human liver protein map: a reference database established by
RT microsequencing and gel comparison.";
RL Electrophoresis 13:992-1001(1992).
RN [8]
RP PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.
RC TISSUE=Keratinocytes;
RX MEDLINE=93162043; PubMed=1286667;
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
RA Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
RT protein database of normal human epidermal keratinocytes.";
RL Electrophoresis 13:960-969(1992).
RN [9]
RP SEQUENCE OF 18-26.
RC TISSUE=Colon carcinoma;
RX MEDLINE=97295306; PubMed=9150948;
RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
RT "A two-dimensional gel database of human colon carcinoma proteins.";
RL Electrophoresis 18:605-613(1997).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -!- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE THE RO AUTOANTIGEN.
CC -----
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DR EMBL; M84739; AAA51916.1; -.
DR EMBL; M32294; AAA36582.1; -.
DR EMBL; AD000092; AAB51176.1; -.
DR PIR; A37047; A37047.
DR PIR; S11475; S11475.
DR PIR; A42330; A42330.
DR PIR; A46452; A46452.
DR SWISS-2DPAGE; P27797; HUMAN.
DR Aarhus/Ghent-2DPAGE; 9401; IEF.
DR HSC-2DPAGE; P27797; HUMAN.
DR MIN; 109091; -.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER-TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1
FT CHAIN 18 417 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 417 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT REPEAT 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 414 417 PREVENT SECRETION FROM ER.
FT CONFLICT 35 35 MISSING (LN REF. 3)
SQ SEQUENCE 417 AA; 48141 MW; BC37C3C0F1054FB2 CRC64;

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Query Match 100.0%; Score 180; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 5e-178;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPAYYFKQFLDGGWTSRWTESKHSKDFGKLVSSGKFGYDEEKDKGLQTSQDARFYAL 60
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Db 18 EPAYYFKQFLDGGWTSRWTESKHSKDFGKLVSSGKFGYDEEKDKGLQTSQDARFYAL 77
    |||

Qy 61 SASPEPFSKGTLLVQQTVAHQEINIDGGGVKVLFPNSLDQTMHGDSSEYNIMFGPDIC 120
    |||
Db 78 SASPEPFSKGTLLVQQTVAHQEINIDGGGVKVLFPNSLDQTMHGDSSEYNIMFGPDIC 137
    |||

Qy 121 GPGTKKVVHVFYKGNVLYNKDKRCKDDETHLYTLVLRPDNTYEVKIDNSQVSGSLE 180
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Db 138 GPGTKKVVHVFYKGNVLYNKDKRCKDDETHLYTLVLRPDNTYEVKIDNSQVSGSLE 197
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RESULT 2
CRTC_MOUSE STANDARD; PRT; 416 AA.
AC P14211;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)

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DE GN CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.; AND SEQUENCE OF 18-48 AND 129-161.
RC STRAIN=BALB/C; TISSUE=Liver;
RX MEDLINE-9005955; PubMed=2563110;
RA Smith M.J.; Koch G.L.E.;
RT "Multiple zones in the sequence of calreticulin (CRP55, calregulin,
RL HACBP), a major calcium binding ER/SR protein.";
RN EMBL J. 8:3581-3586(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-93013037; PubMed=1398135;
RA Mazzarella R.A.; Gold P.; Cunningham M.; Green M.;
RT "Determination of the sequence of an expressible cDNA clone encoding
RL ERP60/calregulin by the use of a novel nested set method.";
RN Gene 120:217-225(1992).
RN [3]
RP SEQUENCE OF 18-38.
RC TISSUE=Fibroblast;
RX MEDLINE-95009907; PubMed=7523108;
RA Merrick B.A.; Patterson R.M.; Wichter L.L.; He C.; Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins,
using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
    LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
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    or send an email to license@isb-sib.ch).

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FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 413 416 PREVENT SECRETION FROM ER.
SQ SEQUENCE 416 AA; 47994 MW; 24C03B00913408D8 CRC64;

Query Match 42.8%; Score 77; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 9e-72;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 DMHGDSEYNIMFGDTCGPGTKKVHVFYFNKGNVLNKDIRCKDDFTHLYTLIVRPDN 163
DB 121 DMHGDSEYNIMFGDTCGPGTKKVHVFYFNKGNVLNKDIRCKDDFTHLYTLIVRPDN 180
QY 164 TYEVKIDNSQVESGSLE 180
DB 181 TYEVKIDNSQVESGSLE 197

RESULT 3
CRTC_RAT
ID CRTC_RAT STANDARD; PRT; 416 AA.
AC P18418; P10452;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (CALBP)
DE (CALCIUM-BINDING PROTEIN 3) (CABP3).
GN CALR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain cortex;
RX MEDLINE=90370496; PubMed=2395661;
RA Murthy K.K., Banville D., Srikanth C.B., Carrier F., Bell A.,
RA Holmes C., Patel Y.C.;
RT "Structural homology between the rat calreticulin gene product and
RL the Onchocerca volvulus antigen Rel-1."
RL Nucleic Acids Res. 18:4933-4933(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=93202172; PubMed=8453984;
RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K.,
RA Okinaga S., Kobayashi T.;
RT "An endoplasmic reticulum protein, calreticulin, is transported into
RL the acrosome of rat sperm."
RL Exp. Cell Res. 205:101-110(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RX MEDLINE=95181573; PubMed=7876339;
RA Soennichsen B., Fueflekrug J., van Nguyen P., Diekmann W.,
RA Robinson D.G., Mieskes G.;
RT "Retention and retrieval: both mechanisms cooperate to maintain
RL calreticulin in the endoplasmic reticulum."
RL J. Cell Sci. 107:2705-2717(1994).
RN [4]
RP SEQUENCE OF 270-358 FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Lone Y.C., Bailly A., Latruffe N.;
RL Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 18-29.
RX MEDLINE=91054414; PubMed=2241926;
RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
RA MacLennan D.H., Meldolesi J., Pozzan T.;
RT "Calreticulin is a candidate for a calsequestrin-like function in
RL Ca2(+)-storage compartments (calcosomes) of liver and brain."
RL Biochem. J. 271:473-480(1990).

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RN [6]
RP SEQUENCE OF 18-32.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Testis;
RX MEDLINE=92360010; PubMed=1497655;
RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;
RT "Calreticulin is present in the acrosome of spermatids of rat
RL testis."
RL Biochem. Biophys. Res. Commun. 186:668-673(1992).
RN [7]
RP SEQUENCE OF 18-32.
RC STRAIN=LEC; TISSUE=Liver;
RX MEDLINE=94072621; PubMed=8251535;
RA Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,
RA Kamataki T.;
RT "Identification of protein disulfide isomerase and calreticulin as
RL autoimmune antigens in LEC strain of rats."
RL Biochim. Biophys. Acta 1158:339-344(1993).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -1- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE D-BETA-
CC HYDROXYBUTYRATE DEHYDROGENASE.
CC -----
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CC -----
DR EMBL; D78308; BAA11345.1;
DR EMBL; X53363; CAA37446.1;
DR EMBL; X13702; CAA31987.1; ALT_SEQ.
DR EMBL; X79327; CAA35890.1;
DR PIR; S04867; S04867.
DR PIR; S11205; S11205.
DR PIR; S13045; S13045.
DR PIR; A49176; A49176.
DR PIR; S45036; S45036.
DR PIR; JH0819; JH0819.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 416 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 416 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 413 416 PREVENT SECRETION FROM ER.
SQ SEQUENCE 416 AA; 47995 MW; 2E6713CED31A2970 CRC64;

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Query Match 42.8%; Score 77; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 9e-72;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 DMHGDSEYNIMFGPDICGPGTKKVVIFNYKGNVINKDKCKDETHLYTLIVRPD 163
DB 121 DMHGDSEYNIMFGPDICGPGTKKVVIFNYKGNVINKDKCKDETHLYTLIVRPD 180

QY 164 TVEVKIDNSQVESGSLE 180
DB 181 TVEVKIDNSQVESGSLE 197

RESULT 4
CRTC_RABIT
ID CRTC_RABIT STANDARD; PRT; 418 AA.
AC P15253;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP). (ERP60).
GN CALR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Slow-twitch skeletal muscle;
RX MEDLINE-90094320; PubMed-2600080;
RA Fliegel L., Burns K., MacLennan D.H., Reithmeier R.A.F., Michalak M.;
RT "Molecular cloning of the high affinity calcium-binding protein
(calreticulin) of skeletal muscle sarcoplasmic reticulum.";
RL J. Biol. Chem. 264:21522-21528(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Fast-twitch skeletal muscle;
RX MEDLINE-91282795; PubMed-2059224;
RA Fliegel L., Michalak M.;
RT "Fast-twitch and slow-twitch skeletal muscles express the same
isoform of calreticulin.";
RL Biochem. Biophys. Res. Commun. 177:979-984(1991).
RN [3]
RP SEQUENCE OF 18-36.
RX MEDLINE-91054414; PubMed-2241926;
RA Través S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
RA MacLennan D.H., Meldolesi J., Pozzan T.;
RT "Calreticulin is a candidate for a calsequestrin-like function in
Ca2(+)-storage compartments (calciosomes) of liver and brain.";
RL Biochem. J. 271:473-480(1990).
RN [4]
RP SEQUENCE OF 18-46.
RX MEDLINE-91201375; PubMed-2016321;
RA Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,
RA Vance J.E., Opas M., Michalak M.;
RT "Calreticulin, and not calsequestrin, is the major calcium binding
protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic
reticulum.";
RL J. Biol. Chem. 266:7155-7165(1991).
RN [5]
RP PARTIAL SEQUENCE.
RC TISSUE-Lung;
RX MEDLINE-92002038; PubMed-1911780;
RA Guan S., Falick A.M., Williams D.E., Cashman J.R.;
RT "Evidence for complex formation between rabbit lung flavin-containing
monooxygenase and calreticulin.";
CC Biochemistry 30:9892-9900(1991).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

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EMBL: J05138; AAA31188.1; -
DR PIR: A34154; A34154.
DR PIR: C33208; C33208.
DR PIR: D33208; D33208.
DR PIR: E33208; E33208.
DR PIR: F33208; F33208.
DR PIR: S13046; S13046.
DR PIR: S13047; S13047.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; Calreticulin; 1.
DR PROSITE: PS000014; ER_TARGET; 1.
DR PROSITE: PS008003; CALRETICULIN_1; 1.
DR PROSITE: PS008004; CALRETICULIN_2; 1.
DR PROSITE: PS008005; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 418 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 418 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 415 418 PREVENT SECRETION FROM ER.
FT VARIANT 35 35 E -> D.
FT CONFLICT 90 90 P -> T (IN REF. 5).
SQ SEQUENCE 418 AA; 48275 MW; B6082B689DC763A6 CRC64;

Query Match 42.8%; Score 77; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 9e-72;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 DMHGDSEYNIMFGPDICGPGTKKVVIFNYKGNVINKDKCKDETHLYTLIVRPD 163
DB 121 DMHGDSEYNIMFGPDICGPGTKKVVIFNYKGNVINKDKCKDETHLYTLIVRPD 180
QY 164 TVEVKIDNSQVESGSLE 180
DB 181 TVEVKIDNSQVESGSLE 197

RESULT 5
CRTL_BOVIN
ID CRTL_BOVIN STANDARD; PRT; 400 AA.
AC P52193;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE CALRETICULIN, BRAIN ISOFORM 1 (CRP55) (CALREGULIN) (HACBP).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bos.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Small intestine;
 RX MEDLINE=96327607; PubMed=8672129;
 RA Winterroo A.K., Fredholm M., Davies W.;
 RT "Evaluation and characterization of a porcine small intestine cDNA
 RL library: analysis of 839 clones.";
 Mamm. Genome 7:509-517(1996).
 [2]
 RP SEQUENCE OF 18-32.
 RX TISSUE=Uterus;
 RC MEDLINE=91201375; PubMed=2016321;
 RA Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,
 Vance J.E., Opas M., Michalak M.;
 RT "Calreticulin, and not calsequestrin, is the major calcium binding
 RT protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic
 RL reticulum.";
 J. Biol. Chem. 266:7185-7165(1991).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

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 CC EMBL; F14591; CAA23142.1; -;
 DR PIR; B33208;
 DR InterPro; IPR001580; Calreticulin.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRODOM; PD001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; PARTIAL.
 DR PROSITE; PS00804; CALRETICULIN_2; PARTIAL.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; PARTIAL.
 KW Endoplasmic reticulum; Calcium-binding; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 >105 CALRETICULIN.
 FT DOMAIN 18 >105 N-DOMAIN.
 FT NON_TER 105 105
 FT SEQUENCE 105 AA; 11958 MW; D203B53FE36BDE1E CRC64;

Query Match 13.9%; Score 25; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.3e-18;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 64 PEPFSNKGQTLVQFTVKHEQNIDC 88
 DB 81 PEPFSNKGQTLVQFTVKHEQNIDC 105
 |||||

RESULT 8
 RALL_ONCVO
 ID RALL_ONCVO STANDARD; PRT; 388 AA.
 AC P11012;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE RAL-1 PROTEIN PRECURSOR (41 KDA LARVAL ANTIGEN).
 GN RALL.
 OS Onchocerca volvulus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 OC Onchocercidae; Onchocerca.
 OX NCBI_TaxID=6282;

RN SEQUENCE FROM N.A.
 RP MEDLINE=94341871; PubMed=7520419;
 RA Rokeach L.A., Zimmerman P.A., Unnasch T.R.;
 RT "Epitopes of the Onchocerca volvulus Rall antigen, a member of the
 RT calreticulin family of proteins, recognized by sera from patients
 RT with onchocerciasis.";
 RL Infect. Immun. 62:3696-3704(1994).
 [2]
 RP SEQUENCE OF 53-388 FROM N.A.
 RX MEDLINE=88273584; PubMed=2455736;
 RA Unnasch T.R., Gallin M.F., Soboslay P.T., Ertmann K.D., Greene B.M.;
 RT "Isolation and characterization of expression cDNA clones encoding
 RT antigens of Onchocerca volvulus infective larvae.";
 RL J. Clin. Invest. 82:262-269(1988).
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

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 CC EMBL; M20565; AAA59056.1; -;
 DR PIR; A32507;
 DR InterPro; IPR001580; Calreticulin.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR PRODOM; PD001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 KW Calcium-binding; Repeat; Antigen; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 388 RAL-1 PROTEIN.
 FT DOMAIN 189 253 4 X APPROXIMATE REPEATS.
 FT REPEAT 189 200 1-1.
 FT REPEAT 208 219 1-2.
 FT REPEAT 225 236 1-3.
 FT REPEAT 242 253 1-4.
 FT DOMAIN 257 295 3 X APPROXIMATE REPEATS.
 FT REPEAT 271 281 2-1.
 FT REPEAT 285 295 2-2.
 FT REPEAT 353 388 ARG/LYS-RICH (BASIC).
 FT DOMAIN 135 161 BY SIMILARITY.
 FT DISULFID 135 161
 FT SEQUENCE 388 AA; 45298 MW; 9537F298A2D31CD6 CRC64;
 SQ
 Query Match 10.6%; Score 19; DB 1; Length 388;
 Best Local Similarity 100.0%; Pred. No. 5.8e-12;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 IMFGPDICGPGTKKVHVIF 131
 DB 128 IMFGPDICGPGTKKVHVIF 146
 |||||

RESULT 9
 CRTC_DROME
 ID CRTC_DROME STANDARD; PRT; 406 AA.
 AC P29413; OSVHA3;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP).
 GN CRC OR CG9429.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.

RX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=93208374; PubMed=1296819;
 RX Smith M.J.;
 RA "Nucleotide sequence of a Drosophila melanogaster gene encoding a
 RT calreticulin homologue.";
 RL DNA Seq. 3:247-250(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Calle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang O., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Anelli J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Fabros B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [3]
 RP SEQUENCE OF 91-124 AND 182-220.
 RX MEDLINE=90307981; PubMed=2365822;
 RA McCauliffe D.P., Zappi E., Lieu T.S., Michalak M., Sontheimer R.D.,
 RA Capra J.D.;
 RA "A human RC/SS-A autoantigen is the homologue of calreticulin and is
 RT highly homologous with oncofetal RAL-1 antigen and an aplasia
 RT 'memory molecule'";
 RL J. Clin. Invest. 86:332-335(1990).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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 CC -----
 CC EMBL; X64461; CAA45791.1; .

DR EMBL; AE003683; AAF54416.1; -.
 DR PIR; A37158; A37158.
 DR FlyBase; FBgn0005585; Crc.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR000886; ER_target.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER_TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 406 CALRETICULIN.
 FT CONFLICT 107 107 G -> A (IN REF. 3).
 FT CONFLICT 184 184 V -> L (IN REF. 3).
 SQ SEQUENCE 406 AA; 46808 MW; 65D72C69D0BEC427 CRC64;

Query Match 10.6% Score 19; DB 1; Length 406;
 Best Local Similarity 100.0%; Pred. No. 6e-12;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 113 IMFGPDICGPGTKKVHVIF 131
 |||||
 DB 130 IMFGPDICGPGTKKVHVIF 148

Search completed: January 14, 2002, 08:51:32
 Job time: 118 sec

GenCore.version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
OM protein - protein search, using sw model
Run on: January 14, 2002, 08:50:09 ; Search time 23.48 Seconds
(without alignments)
1121.338 Million cell updates/sec
Title: US-09-828-000-3
Perfect score: 180
Sequence: 1 EPAYVKEQFLDGDGWTGRW.....PONTVEYKIDNSQVSGSLE 180
Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 473505 seqs, 146272329 residues
Word size : 18
Total number of hits satisfying chosen parameters: 11
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 45 summaries

Database : SPTREMBL17.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Match Length DB ID	Description
1	27	15.0 214 4	Q9UDG2 homo sapien
2	27	15.0 405 5	Q26268 aplysia cal
3	27	15.0 421 5	Q9u6S0 strongyloce
4	25	13.9 318 13	Q9PTX7 lampetra re
5	24	13.3 410 5	Q16893 amblyomma a
6	22	12.2 343 13	Q91711 xenopus lae
7	22	12.2 411 13	Q91710 xenopus lae
8	21	11.7 387 5	Q97372 dirofilaria
9	20	11.1 419 13	Q98984 rana rugosa
10	19	10.6 375 5	Q18478 litomosolide
11	19	10.6 406 5	Q9u916 drosophila

ALIGNMENTS
RESULT 1
Q9UDG2 PRELIMINARY; PRT; 214 AA.

AC Q9UDG2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CALRETICULIN-CALCIUM BINDING PROTEIN (FRAGMENTS).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95143082; PubMed=7841019;
RA Houen G., Koch C.;
RT "Human placental calreticulin: purification, characterization and association with other proteins";
RL Acta Chem. Scand. 48:905-911(1994).
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 3.
DR ProDom; PD001866; Calreticulin; 1.
FT NON_TER 1 1
FT NON_CONS 31 32
FT NON_CONS 59 60
FT NON_CONS 78 79
FT NON_CONS 116 117
FT NON_TER 214 214
SQ SEQUENCE 214 AA; 24341 MW; AC9269459C1356BE CRC64;

Query Match 15.0%; Score 27; DB 4; Length 214;
Best Local Similarity 100.0%; Pred. No. 4e-21;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPAYVKEQFLDGDGWTGRWIESKHKS 27
Db 1 EPAYVKEQFLDGDGWTGRWIESKHKS 27
RESULT 2
Q26268
ID Q26268 PRELIMINARY; PRT; 405 AA.
AC Q26268;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CALRETICULIN
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidia;
OC Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93098937; PubMed=1463604;
RA Kennedy T.E., Kuhl D., Barzilai A., Sweatt J.D., Kandel E.R.;
RT "Long-term sensitization training in Aplysia leads to an increase in calreticulin, a major presynaptic calcium-binding protein.";
RL Neuron 9:1013-1024(1992).
DR EMBL; S51239; AAB24569.1; -;
DR InterPro; IPR000886; ER_target.
DR ProDom; PD001866; Calreticulin; 1.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 405 AA; 46738 MW; 14CAA201840D1D69 CRC64;

Query Match 15.0%; Score 27; DB 5; Length 405;
Best Local Similarity 100.0%; Pred. No. 6.8e-21;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 YNMFPGDICGPGTKKVVHVFYKGN 137
 DB 124 YNMFPGDICGPGTKKVVHVFYKGN 150

RESULT 3
 ID Q9U6S0 PRELIMINARY; PRT; 421 AA.
 AC Q9U6S0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE CALRETICULIN PRECURSOR.
 GN CALRET.
 OS Strongylocentrotus purpuratus (Purple sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinozoa; Echinozoa; Echinacea; Echinoida; Strongylocentrotidae;
 OC Strongylocentrotus.
 OX NCBI_TaxID=7668;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Susan J.M., Just M.L., Lonnarz W.J.;
 RT "Cloning and Characterization of Alpha Integrin and Calreticulin in
 Embryos of the Sea Urchin.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DE EMBL: AF177915; AAD55725.1; -;
 DR InterPro: IPR000886; ER_target.
 DR InterPro: IPR001580; Calreticulin.
 DR Pfam: PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR ProSITE; PS00804; CALRETICULIN.2; 1.
 DR ProSITE; PS00805; CALRETICULIN_REPEAT; 3.
 DR ProSITE; PS00014; ER_TARGET; UNKNOWN_1.
 KW Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 421 CALRETICULIN.
 FT TAG 421
 SQ SEQUENCE 421 AA; 48822 MW; 172C664F59F41F93 CRC64;

Query Match 15.0%; Score 27; DB 5; Length 421;
 Best Local Similarity 100.0%; Pred. No. 7e-21;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 YNMFPGDICGPGTKKVVHVFYKGN 137
 DB 127 YNMFPGDICGPGTKKVVHVFYKGN 153

RESULT 4
 ID Q9PTX7 PRELIMINARY; PRT; 318 AA.
 AC Q9PTX7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE CALRETICULIN (FRAGMENT).
 OS Lampetra reissneri.
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzontidae; Lampetra.
 OX NCBI_TaxID=7753;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-20063780; PubMed:10594174;
 RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
 RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
 genes.";
 RL J. Mol. Evol. 49:729-735(1999).
 DR EMBL: AB025328; BAA88481.1; -;
 DR InterPro: IPR000886; ER_target.
 DR InterPro: IPR001580; Calreticulin.
 DR Pfam: PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.

DR ProDom; PD001866; Calreticulin; 1.
 DR ProSITE; PS00804; CALRETICULIN.2; 1.
 DR ProSITE; PS00805; CALRETICULIN_REPEAT; 3.
 DR ProSITE; PS00014; ER_TARGET; UNKNOWN_1.
 FT NON_TER 1
 SQ SEQUENCE 318 AA; 36997 MW; C88102EALCACL1506 CRC64;

Query Match 13.9%; Score 25; DB 13; Length 318;
 Best Local Similarity 100.0%; Pred. No. 8.4e-19;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 IMFGPDICGPGTKKVVHVFYKGN 137
 DB 29 IMFGPDICGPGTKKVVHVFYKGN 53

RESULT 5
 ID Q16893 PRELIMINARY; PRT; 410 AA.
 AC Q16893;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE CALRETICULIN.
 GN CRT-1.
 OS Amblyomma americanum.
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 OC Parasitiformes; Ixodida; Ixodidae; Amblyomma.
 OX NCBI_TaxID=6943;
 RN [1]
 RP SEQUENCE OF 49-410 FROM N.A.
 RC TISSUE-SALIVARY GLANDS;
 RA Jaworski D.C., Simmen F.A., Lamoreaux W.J., Coons L.B., Muller M.T.,
 RT Needham G.R.;
 RT "A secreted calreticulin protein in Ixodid tick (Amblyomma americanum)
 RT saliva.";
 RL J. Insect Physiol. 41:369-375(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SALIVARY GLANDS;
 RA Jaworski D.C.;
 RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SALIVARY GLANDS;
 RA Fain-Thornton J.M., Jaworski D.C., Needham G.R.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U07708; AAC79094.1; -;
 DR InterPro: IPR000886; ER_target.
 DR InterPro: IPR001580; Calreticulin.
 DR Pfam: PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR ProSITE; PS00803; CALRETICULIN.1; 1.
 DR ProSITE; PS00805; CALRETICULIN_REPEAT; 3.
 DR ProSITE; PS00014; ER_TARGET; UNKNOWN_1.
 SQ SEQUENCE 410 AA; 47485 MW; 32CCB8750A17DC54 CRC64;

Query Match 13.3%; Score 24; DB 5; Length 410;
 Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 TLVVQFTVKHEQNIDCGGVYKLF 96
 DB 89 TLVVQFTVKHEQNIDCGGVYKLF 112

RESULT 6
 Q91711 PRELIMINARY; PRT; 343 AA.
 ID Q91711
 AC Q91711;

DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CALRETICULIN (FRAGMENT).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=93074997; PubMed=1445218;
RA Treves S., Zorzato F., Pozzan T.;
RT "Identification of calreticulin isoforms in the central nervous
system.";
RL Biochem. J. 287:579-581(1992).
DR EMBL; X67598; CAA47867.1; -.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
FT NON_TER 1
FT NON_TER 343
FT SIGNAL 343
SQ SEQUENCE 343 AA; 40105 MW; 3E7DDAFA33B91DE1 CRC64;

Query Match 12.2%; Score 22; DB 13; Length 343;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 FTHLYTLIVRPDNTYEVKIDNS 172
Db 140 FTHLYTLIVRPDNTYEVKIDNS 161
|||||

RESULT 7
ID Q91710 PRELIMINARY; PRT; 411 AA.
AC Q91710;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CALRETICULIN PRECURSOR (FRAGMENT).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=93074997; PubMed=1445218;
RA Treves S., Zorzato F., Pozzan T.;
RT "Identification of calreticulin isoforms in the central nervous
system.";
RL Biochem. J. 287:579-581(1992).
DR EMBL; X67597; CAA47866.1; -.
DR InterPro: IPR000886; ER.target.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Signal.
FT NON_TER 1
FT NON_TER 12
FT SIGNAL <1 12 POTENTIAL.

FT CHAIN 13 411 CALRETICULIN.
SQ SEQUENCE 411 AA; 48344 MW; 891DA66E00EBBEFA CRC64;

Query Match 12.2%; Score 22; DB 13; Length 411;
Best Local Similarity 100.0%; Pred. No. 1.9e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 FTHLYTLIVRPDNTYEVKIDNS 172
Db 163 FTHLYTLIVRPDNTYEVKIDNS 184
|||||

RESULT 8
ID Q97372 PRELIMINARY; PRT; 387 AA.
AC Q97372;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CALRETICULIN PRECURSOR.
OS Dirofilaria immitis.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Dirofilaria.
OX NCBI_TaxID=6287;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99094497; PubMed=9879888;
RA Tsuji N., Morales T.H., Ozols V.V., Carmody A.B., Chandrashekar R.;
RT "Molecular characterization of a calcium-binding protein from the
filarial parasite Dirofilaria immitis.";
RL Mol. Biochem. Parasitol. 97:69-79(1998).
DR EMBL; AF052978; AAD03405.1; -.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 387 CALRETICULIN.
SQ SEQUENCE 387 AA; 44941 MW; E7741BF6AAFA5885 CRC64;

Query Match 11.7%; Score 21; DB 5; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.3e-14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 YNIMFGPDICGPGTKKVHVIF 131
Db 126 YNIMFGPDICGPGTKKVHVIF 146
|||||

RESULT 9
ID Q98984 PRELIMINARY; PRT; 419 AA.
AC Q98984;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CALRETICULIN.
OS Rana rugosa (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96234004; PubMed=8654561;
RA Yamamoto S., Nakamura M.;
RT "Calnexin: its molecular cloning and expression in the liver of the
frog, Rana rugosa.";

RL FEBS Lett. 387:27-32(1996).

RN [2]

RP SEQUENCE FROM N.A.

RA Yamamoto S.;

RT "Strong expression of the calreticulin gene in the liver of Rana

RL J. Exp. Zool. 0:0-0(1996).

DR EMBL; D78589; BAA11425.1; -.

DR InterPro; IPR000886; ER_target.

DR Pfam; PF00262; calreticulin; 1.

DR PRINTS; PR00626; CALRETICULIN.

DR PRODOM; PD001866; Calreticulin; 1.

DR PROSITE; PS00803; CALRETICULIN_1; 1.

DR PROSITE; PS00804; CALRETICULIN_2; 1.

DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.

DR PROSITE; PS0014; ER_TARGET; UNKNOWN_1.

SQ SEQUENCE 419 AA; 48658 MW; 2C857036769673BF CRC64;

Query Match

Best Local Similarity 11.1%; Score 20; DB 13; Length 419;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 HLYTLVIRPDNTYEVKIDNS 172

DB 171 HLYTLVIRPDNTYEVKIDNS 190

RESULT 10

O18478

ID O18478 PRELIMINARY; PRT; 375 AA.

AC O18478;

DT 01-JAN-1998 (TRENBLrel. 05, Created)

DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)

DE RAL-1 PROTEIN (FRAGMENT).

OS Litomosoides sigmodontis.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;

OC Onchocercidae; Litomosoides.

OX NCBI_TaxID-42156;

RN [1]

RP SEQUENCE FROM N.A.

RA MacLennan K., Hoffman W.H., Taylor D.W.;

RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ001621; CAA04877.1; -.

DR InterPro; IPR001580; Calreticulin.

DR Pfam; PF00262; calreticulin; 1.

DR PRINTS; PR00626; CALRETICULIN.

DR PRODOM; PD001866; Calreticulin; 1.

DR PROSITE; PS00803; CALRETICULIN_1; 1.

DR PROSITE; PS00804; CALRETICULIN_2; 1.

DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.

FT NON_TER 375

SQ SEQUENCE 375 AA; 43842 MW; 03F7642FBFF7A5B8 CRC64;

Query Match

Best Local Similarity 10.6%; Score 19; DB 5; Length 375;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 IMFGPDICGPGTKKVVHVF 131

DB 128 IMFGPDICGPGTKKVVHVF 146

RESULT 11

Q9U916

ID Q9U916 PRELIMINARY; PRT; 406 AA.

AC Q9U916;

DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)

DE CALRETICULIN.

GN CRC OR CG9429.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID-7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-OREGON-R;

RA Dodo K., Sakoyama Y., Gamo S.;

RT "Drosophila melanogaster calreticulin for mRNA.";

RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB000718; BAA85379.1; -.

DR FLYBase; FBgn0005585; CRC.

DR InterPro; IPR001580; Calreticulin.

DR InterPro; IPR000886; ER_target.

DR Pfam; PF00262; calreticulin; 1.

DR PRINTS; PR00626; CALRETICULIN.

DR PRODOM; PD001866; Calreticulin; 1.

DR PROSITE; PS00803; CALRETICULIN_1; 1.

DR PROSITE; PS00804; CALRETICULIN_2; 1.

DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.

DR PROSITE; PS0014; ER_TARGET; UNKNOWN_1.

SQ SEQUENCE 406 AA; 46809 MW; 68BA49A6B81CC427 CRC64;

Query Match

Best Local Similarity 10.6%; Score 19; DB 5; Length 406;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 IMFGPDICGPGTKKVVHVF 131

DB 130 IMFGPDICGPGTKKVVHVF 148

Search completed: January 14, 2002, 08:52:02

Job time: 113 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 9, 2002, 14:58:34 ; Search time 83.2 Seconds
(without alignments)
160.255 Million cell updates/sec

Title: US-09-828-000-3
Perfect score: 971
Sequence: 1 EPAYPKFQLDGDGWTSRW.....PONTYEVKIDNSQVESGSLE 180

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_1101.*
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2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
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21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	971	100.0	180	21	Human vasostatin (
2	971	100.0	400	21	Recombinant human
3	971	100.0	417	10	60 kD Ro (Ro/SSA)
4	971	100.0	417	21	Human MBP-calretic
5	966	99.5	417	20	Calreticulin. Hom
6	921	94.9	401	18	Calreticulin. Hom
7	700	72.1	403	17	Flea calreticulin
8	631	65.0	385	21	Human secreted pro
9	541.5	55.8	336	12	Partial sequence o
10	527	54.3	415	22	Castor bean calret
11	527	54.3	415	22	Castor bean calret

12	510	52.5	421	21	AAG24608	Arabidopsis thalia
13	510	52.5	421	21	AAG47932	Arabidopsis thalia
14	510	52.5	424	21	AAG24607	Arabidopsis thalia
15	510	52.5	424	21	AAG47931	Arabidopsis thalia
16	510	52.5	441	21	AAG30997	Arabidopsis thalia
17	510	52.5	444	21	AAG30996	Arabidopsis thalia
18	327	33.7	61	21	AAI92352	Recombinant human
19	318	32.7	60	21	AAI92354	Recombinant human
20	318	32.7	280	21	AAI92355	Recombinant delta-
21	301.5	31.1	417	21	AAI77953	A. thaliana enviro
22	290	29.9	593	16	AAI71094	Calnexin sequence.
23	258	26.6	49	21	AAI92353	Recombinant human
24	253	26.1	312	21	AAI92353	Arabidopsis thalia
25	253	26.1	312	21	AAG47933	Arabidopsis thalia
26	253	26.1	332	21	AAG30998	Arabidopsis thalia
27	250.5	25.8	84	21	AAG41018	Zea mays protein f
28	238.5	24.6	530	21	AAG26284	Arabidopsis thalia
29	238.5	24.6	530	21	AAG46611	Arabidopsis thalia
30	238.5	24.6	567	21	AAG46610	Arabidopsis thalia
31	227.5	23.4	542	22	AAB66342	Castor bean calnex
32	200.5	20.6	532	21	AAG04448	Arabidopsis thalia
33	200.5	20.6	548	21	AAG04447	Arabidopsis thalia
34	190	19.6	122	20	AAI00924	Human cClqR bindin
35	190	19.6	122	20	AAI00925	Mouse cClqR bindin
36	182	18.7	122	20	AAI00925	Arabidopsis thalia
37	145	14.9	91	21	AAG34014	Arabidopsis thalia
38	145	14.9	99	21	AAG34013	Arabidopsis thalia
39	140.5	14.5	256	22	AAB99168	Human Endoplasmic
40	124.5	12.5	221	21	AAB56468	Human prostate can
41	114.5	11.8	162	21	AAG00147	Human secreted pro
42	114.5	11.8	162	21	AAG00148	Human secreted pro
43	112.5	11.6	394	21	AAG26285	Arabidopsis thalia
44	112.5	11.6	394	21	AAG46612	Arabidopsis thalia
45	110.5	11.4	125	21	AAG25999	Zea mays protein f

ALIGNMENTS

RESULT 1
AAI92351
ID AAI92351 standard; Protein; 180 AA.
XX
AC AAI92351;
XX
DT 10-AUG-2000 (first entry)
XX
DE Human vasostatin (calreticulin N-terminal 180 amino acids).
XX
KW MBP-calreticulin; maltose binding protein; vasostatin; N-terminal; anglogenesis; inhibition; endothelial cell; anti-angiogenic;
KW neuroprotective; antidiabetic; cytostatic; dermatological; hepatic;
KW immunosuppressive; antiinflammatory; anti-atherosclerotic;
KW gastrointestinal; anti-arthritis; ophthalmic.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200020577-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US23240.
XX
PR 06-OCT-1998; 98US-0103438.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Tosato G, Pike SE, Yao L;
XX
DR WPI; 2000-303767/26.
XX
PT Inhibiting endothelial cell growth and angiogenesis using calreticulin.

PT DNA sequences encoding antigenic epitope(s) of Ro 60 kD autoantigen
 PT - used in immunoassays to detect rheumatic disease
 XX Disclosure; Fig 2; 88pp; English.
 CC Synthetic peptides corresp. to an epitopic core of Ro antigen are
 CC expressed recombinantly to detect autoantibodies, for identification
 CC of autoimmune diseases. These epitopes are AAs 24-36, 23-36, 188-209,
 CC or 241-255. The peptides may be substd. for ribonucleoprotein particle
 CC antigens.
 XX Sequence 417 AA;
 SQ

Query Match 100.0%; Score 971; DB 10; Length 417;
 Best Local Similarity 100.0%; Pred. No. 9.9e-99;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAYVFEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDEEKDGLQTSQDARFYAL 60
 DB 18 epavyfkeqfldgdgwtswieskhksdfgkflvssgkfygdeekdkqltsqdarfyal 77
 QY 61 SASFEPSNKGQTLVQVFTVKHEQNIDCGGYVKLFPSNLDQTDHGDSEYNIMFGPDIC 120
 DB 78 sasfepfsnkgqtlvvqftvkheqndicgggyvklfpsnldqtdmhdseynlmfgpdic 137
 QY 121 GPGTKKVHVIFNKGKLVINKDIRCKDDEFTHLTYTLIVRPDNTYEVKIDNSQVESGSL 180
 DB 138 gpgtkkvhvifnykgknlvinkdirckddeftthlytlivrpndtyevkidnsqvesgsle 197

RESULT 4
 AAY92349
 ID AAY92349 standard; Protein; 417 AA.
 XX
 AC AAY92349;
 XX
 DT 10-AUG-2000 (first entry)
 XX
 DE Human MBP-calreticulin.
 XX
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..17
 FT /label= signal_peptide
 FT Protein 18
 FT /label= mature_protein
 XX
 PN WO200020577-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 05-OCT-1999; 99WO-0523240.
 XX
 PR 06-OCT-1998; 98US-0103438.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Tosato G, Pike SE, Yao L;
 XX WPI: 2000-303767/26.
 DR N-PSDB; AAA09346, AAA09347.
 XX
 XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth
 XX
 PS Disclosure; Page 79-80; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises
 CC contacting the cells with calreticulin (or its fragments/variants).
 CC fragments of calreticulin causes at least 40% inhibition of angiogenesis,
 CC tumor growth and/or endothelial cell growth (claimed). The method may be
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is
 CC associated with a disease other than a tumor that is associated with
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
 CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune
 CC inflammation, atherosclerosis, excessive wound repair, retinal
 CC neovascularization, macular degeneration, corneal graft rejection,
 CC contact lens overwear, Crohn's disease, non-immune inflammation,
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
 CC also be used for treating/inhibiting tumor growth especially
 CC Kaposi's sarcoma (claimed).
 XX Sequence 417 AA;
 SQ

Query Match 100.0%; Score 971; DB 21; Length 417;
 Best Local Similarity 100.0%; Pred. No. 9.9e-99;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAYVFEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDEEKDGLQTSQDARFYAL 60
 DB 18 epavyfkeqfldgdgwtswieskhksdfgkflvssgkfygdeekdkqltsqdarfyal 77
 QY 61 SASFEPSNKGQTLVQVFTVKHEQNIDCGGYVKLFPSNLDQTDHGDSEYNIMFGPDIC 120
 DB 78 sasfepfsnkgqtlvvqftvkheqndicgggyvklfpsnldqtdmhdseynlmfgpdic 137
 QY 121 GPGTKKVHVIFNKGKLVINKDIRCKDDEFTHLTYTLIVRPDNTYEVKIDNSQVESGSL 180
 DB 138 gpgtkkvhvifnykgknlvinkdirckddeftthlytlivrpndtyevkidnsqvesgsle 197

RESULT 5
 AAY00927
 ID AAY00927 standard; Protein; 417 AA.
 XX
 AC AAY00927;
 XX
 DT 28-MAY-1999 (first entry)
 XX
 DE Calreticulin.
 XX
 KW Clq and collectin receptor; cClqR binding domain; complement ubiquitin;
 KW CUB functionality; inhibitor; complement activation; inflammation;
 KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
 KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
 KW immune complex nephritis; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO9907406-A1.
 XX
 PD 18-FEB-1999.
 XX
 PF 12-AUG-1998; 98WO-GB02430.
 XX
 PR 12-AUG-1997; 97GB-0016998.
 XX
 PA (UYLE-) UNIV LEICESTER.
 XX
 PI Schwaebler W;
 XX WPI: 1999-180404/15.
 DR
 XX Use of a cClqR binding domain - to modulate complement ubiquitin
 PT (CUB) functionality.
 XX

PS Disclosure; Page 26-27; 31pp; English.

XX This sequence is calreticulin, a homologue of C1q and collectin receptor (cC1qR). The invention relates to the use of a cC1qR binding domain in a medicament to effect complement ubiquitin (CUB) functionality, and an inhibitor of the cC1qR binding domain in a medicament to inhibit CUB functionality. The cC1qR binding domain, or its inhibitor, can be used to treat a human or animal body. Particularly an inhibitor is used to treat complement activation involved in the initiation and maintenance of inflammation, for example in myocardial infarction, brain ischaemia (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus erythematosus, burns, immune complex nephritis, and to treat amyloid plaques in Alzheimer's disease. The use of cC1qR binding domain or inhibitor enables the CUB domain functionality to be modulated using a low molecular weight molecule.

XX Sequence 417 AA;

Query Match 99.5%; Score 966; DB 20; Length 417;
Best Local Similarity 99.4%; Pred. No. 3.5e-98;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EPAYVKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDDEKDKGLQTSQDARFYAL 60
DB 18 epavykqefldgdgwtprwieskhksdfgkflvssgkfygdeekdkglqtsqdarfyal 77
QY 61 SASFEPFSNKGQFLVQVFTVKHEQNIDCGGYVKLFPNSLDQTDHGDSEYNTMFGPDIC 120
DB 78 sasfepfsnkgqflvvqftvkheqndcgggyvklfpnsldqtdhgdseynlmfpgdic 137
QY 121 GPCTKKVHVIFNYKGNVLINKDIRCKDDEFTHLVLPDNTYEVKIDNSOVESGSLE 180
DB 138 gptckkvhvfnykgnvlinkdirckddeftthlylvprpntyevkidnsqvesgsle 197

RESULT 6

ID AAW11156 standard; peptide; 401 AA.

AC AAW11156;

DT 31-MAY-1997 (first entry)

DE Calreticulin.

KW calreticulin; C-domain; restenosis; inhibitor.

OS Homo sapiens.

PN WO9636643-A1.

PD 21-NOV-1996.

PF 17-MAY-1996; 96WO-IB00471.

PR 16-MAY-1996; 96US-0649417.

PR 17-MAY-1995; 95US-0442844.

XX (UYAL-) UNIV ALBERTA.

XX Lucas A, Michalak M;

DR WPI; 1997-012036/01.

XX Inhibition of restenosis in patients - using calreticulin or a C-domain polypeptide of calreticulin or a variant with the same activity.

PS Disclosure; Fig 1; 48pp; English.

XX The present sequence is calreticulin. It and a C-domain derived peptide (AAW06736) are useful for treating a patient to inhibit restenosis. The

CC calreticulin-type cpds. are administered either parenterally,
CC intravenously or via a catheter and can target areas of vascular damage
CC to inhibit or prevent restenosis.

XX Sequence 401 AA;

Query Match 94.9%; Score 921; DB 18; Length 401;
Best Local Similarity 95.0%; Pred. No. 3.1e-93;
Matches 171; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 EPAYVKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDDEKDKGLQTSQDARFYAL 60

DB 1 epvyvkeqfldgdgwtserwieskhksdfgkflvssgkfygdeekdkglqtsqdarfyal 60

QY 61 SASFEPFSNKGQFLVQVFTVKHEQNIDCGGYVKLFPNSLDQTDHGDSEYNTMFGPDIC 120

DB 61 sarfepfsnkgqflvvqftvkheqndcgggyvklfpagldqtdhgdseynlmfpgdic 120

QY 121 GPCTKKVHVIFNYKGNVLINKDIRCKDDEFTHLVLPDNTYEVKIDNSOVESGSLE 180

DB 121 gptckkvhvfnykgnvlinkdirckddeftthlylvprpntyevkidnsqvesgsle 180

RESULT 7

ID AAW04171 standard; Protein; 403 AA.

XX AAW04171;

XX 12-DEC-1996 (first entry)

DE Flea calreticulin PCTCal403.

KW Calreticulin; flea; haematophagous insect; allergic dermatitis;

KW vaccine; therapy; PCTCal403.

OS Ctenocephalides felis.

PN WO9628469-A1.

PD 19-SEP-1996.

PF 08-MAR-1996; 96WO-US03133.

PR 09-MAR-1995; 95US-0401509.

XX (HESK-) HESKA CORP.

XX Rushlow KE, Stiegler GL;

DR WPI; 1996-442861/44.

DR N-PSDB; AAT39516;

DR N-PSDB; AAT39517.

XX Haematophagous insect calreticulin protein - used to reduce insect infestation and desensitise patients to allergic dermatitis

PS Claim 5; Page 68-69; 86pp; English.

XX Flea calreticulin protein PCTCal1589 (AAW04171) is a calcium-binding

CC protein found in the salivary glands of Ctenocephalides felis.

CC Its amino acid sequence was deduced from a cDNA clone (AAT39516)

CC obtd. from a salivary gland cDNA library. Recombinant PCTCal1589

CC can be produced in host cells transformed with a vector carrying

CC calreticulin nucleic acids. Calreticulin alters the blood feeding

CC behaviour of haematophagous insects and can be administered to an

CC animal to reduce infestation. It reduces calreticulin activity in

CC insects, so reducing the insect burden on an animal. Calreticulin

CC can be used to elicit an immune response, thereby desensitising an

CC animal to allergic dermatitis caused by fleas, mosquitoes or

CC Culicoides.

XX

SQ Sequence 403 AA;

Query Match 72.1%; Score 700; DB 17; Length 403;
Best Local Similarity 71.7%; Pred. No. 7.8e-69;
Matches 129; Conservative 23; Mismatches 26; Indels 2; Gaps 2;

QY 2 PAVYFEQFLDGDGWTSRWIESKHK-SDFGKFLVSSGKFGYDEEKDGLQTSQDARFYAL 60
Db 19 pevlfleenfvd-dwtntwvsehpkgefkgfvtgtagkfyndaeackglqtgqdarfyal 77
QY 61 SASFEPFSGKQTLVYQFTVKHEQNIDCGGGYVKLPFNSLDQTDHMGDSYNTMFGPDIC 120
Db 78 shkfpsnkdktlvqfsvkhegnidcggylkgfsvnqkdmhgespyelmfgpdic 137
QY 121 GPCTKKVHVFNKGNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
Db 138 dbpttkkvhwifsykgnvlindirckddvrythvtytlvkvkpdnteyavldnekvsgnle 197

RESULT 8
AAB32385
ID AAB32385 standard; Protein; 385 AA.
XX
AC AAB32385;
XX
DT 16-JAN-2001 (first entry)
XX
DE Human secreted protein sequence encoded by gene 15 SEQ ID NO:71.
XX
KW Human; secreted protein; cytostatic; immunostimulant; antiproliferative;
KW cardiant; antiarrhythmic; antiviral; antibacterial; antifungal; cancer;
KW antiparasitic; neuroprotective; nootropic; antiinflammatory; anti-HIV;
KW antiangiogenic; antiarteriosclerotic; diagnosis; immune disorder; AIDS;
KW autoimmune disease; haematopoietic cell disorder; blood protein disorder;
KW agammaglobulinaemia; hyperproliferative disease; Gaucher's disease;
KW cardiovascular disorder; congenital heart defect; pulmonary atresia;
KW arrhythmia; ischaemia; angiogenesis related disorder; Crohn's disease;
KW atherosclerosis; neurological disease; Alzheimer's disease;
KW Huntington's; infectious disease; cat-scratch disease.
XX
OS Homo sapiens.
XX
PN WO200047602-A1.
XX
PD 17-AUG-2000.
XX
PF 08-FEB-2000; 2000WO-US03062.
XX
PR 10-FEB-1999; 99US-0119468.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Ebner R, Young PE, NI J, Soppet DR, Moore PA;
PI Shi Y, Lafleur DW, Olsen HS, Florence KA, Komatsoulis G;
XX
DR WPI; 2000-543578/49.
DR N-PSDB; AAC55204.
XX
XX New human nucleic acids encoding secreted proteins, useful in the
PT treatment, prevention or diagnosis of immune disorders (e.g. autoimmune
PT diseases), blood protein disorders and hyperproliferative diseases
PT (e.g. Gaucher's disease).
XX
PS Claim 11; Page 434-435; 488pp; English.
XX
CC The polynucleotide sequences given in AAC55190 to AAC55235 encode the
CC human secreted proteins given in AAB32371 to AAB32484. Human secreted
CC proteins have activities based on the tissues and cells the genes are
CC expressed in. Examples of activities include: cytostatic;
CC immunostimulant; antiproliferative; cardiant; antiarrhythmic; antiviral;
CC antibacterial; antifungal; antiparasitic; neuroprotective; nootropic;
CC antiinflammatory; antiangiogenic; anti-HIV; and antiarteriosclerotic. The

CC polynucleotides and polypeptides, or their agonists and antagonists, can
CC be used for treating, preventing or diagnosing immune disorders (e.g.
CC cancer, autoimmune diseases), disorders of haematopoietic cells, blood
CC protein disorders (e.g. agammaglobulinaemia), hyperproliferative
CC diseases (e.g. Gaucher's disease), cardiovascular disorders (e.g.
CC congenital heart defects, pulmonary artery disease, arrhythmias, ischaemia),
CC angiogenesis related disorders (e.g. Crohn's disease, atherosclerosis),
CC neurological diseases (e.g. Alzheimer's disease, Huntington's chorea),
CC infectious diseases (e.g. AIDS, cat-scratch disease and other bacterial,
CC viral, parasitic or fungal diseases), AAC55181 to AAC55189 and AAB32370
CC represent sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 385 AA;

Query Match 65.0%; Score 631; DB 21; Length 385;
Best Local Similarity 64.4%; Pred. No. 3e-61;
Matches 114; Conservative 30; Mismatches 33; Indels 0; Gaps 0;

QY 4 VYFEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDEEKDGLQTSQDARFYALSAS 63
Db 21 vyfgeefldghehwnrwlqstndsrfgfrlrsfgkfyghkekdkglqtqngryfaisar 80²
QY 64 FEPFSGKQTLVYQFTVKHEQNIDCGGGYVKLPFNSLDQTDHMGDSYNTMFGPDICGPG 123
Db 81 fkpfsnkgktlvqytkvheqkmdcgggykvpadidqknlnksgqyymfpgdicgfd 140
QY 124 TKKVHVFNKGNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
Db 141 ikkvhvilhfknyhenkklirckvdfthlytlirpdisydvkldggsiesgsle 197

RESULT 9
AAR12312
ID AAR12312 standard; Protein; 336 AA.
XX
AC AAR12312;
XX
DT 29-AUG-1991 (first entry)
XX
DE Partial sequence of Onchocera volvulus 42 kD antigen.
XX
KW River blindness; onchocerciasis; vaccine; antigen; parasite.
XX
OS Onchocerca volvulus.
XX
FH Key Location/Qualifiers
FT Region 160..166
FT /label= repeat unit
FT /note= "hydrophilic"
FT Region 177..183
FT /label= repeat unit
FT /note= "hydrophilic"
FT Region 195..201
FT /label= repeat unit
FT /note= "hydrophilic"
XX
PN US0201342-A.
XX
XX 04-JUN-1991.
PD
XX 30-JUN-1988; 88US-0214264.
PF
XX 30-JUN-1988; 88US-0214264.
PR
XX (UYHO-) UNIV HOSPITALS CLEV.
PA
XX Greene BM, Unnasch TR;
PI
XX WPI; 1991-185179/25.
DR
DR N-PSDB; AAK11987.
XX

PT DNA encoding Onchocerca volvulus antigen - used to express
PT recombinant antigen for vaccine against onchocerciasis or river
PT blindness.
PS Disclosure; Fig 7; 20pp; English.
PS
XX The sequence was deduced from a cDNA clone lambda RAL-1 prepd.
CC from RNA isolated from nodules excised from patients infected
CC with O. volvulus. The N-terminal is incomplete, however Abs
CC which specifically bind to protein prepd. from induced cultures
CC of lambda RAL-1 lysogens recognise a single polypeptide of mol.
CC wt. 42,000 in extracts of adult worms. Analysis deduced sequence
CC suggests that it encodes a protein of mol. wt. 39,130. If the
CC antigen is not subject to post-translational processing this
CC suggests that most of the coding sequence is present. The three
CC repeats are highly hydrophilic regions likely to be exposed on
CC the surface of the antigen and highly immunogenic. Recombinant
CC antigen expressed by the clone can be used stimulate T-cells of
CC individuals infected by the parasite to proliferate and may be
CC used as the basis for a vaccine against Onchocerciasis or river
CC blindness.
XX Sequence 336 AA;

Query Match 55.8%; Score 541.5; DB 12; Length 336;
Best Local Similarity 68.5%; Pred. No. 1.9e-51;
Matches 98; Conservative 21; Mismatches 23; Indels 1; Gaps 1;
QY 39 FYGDEKKGKGLQTSQDARYALSASF-PFSNKGOTLVVQFTVKHEQNTDCGGYVKLFP 97
Db 1 fygdaavdkglkttqdaakfyslgakfdksfnkgsalvqfsvkheqidecggvkvkima 60
QY 98 NSLDQTMHGDSEYNTMGPDICGPGTKKHVHFYFNKGNVLINKDIRCKDDEFTHLTYL 157
Db 61 sdvnledshgetpyhmimgpdcpgptkvhvifhykdrnmhmkdkirckdadvfthlytl 120
QY 158 IVRPONTYEVKIDNSQVESGSL 180
Db 121 lvsndtyevqldgekaegele 143

RESULT 10
AAB66341
ID AAB66341 standard; Protein; 415 AA.
XX
AC AAB66341;
XX
DT 05-APR-2001 (first entry)
XX
DE Castor bean calreticulin SEQ ID NO: 2.
XX
KW Castor bean; calreticulin; calcium binding; er; endoplasmic reticulum;
KW calnexin; promoter; resistance.
XX
OS Ricinus communis.
XX
PN US6171864-B1.
XX
PD 09-JAN-2001.
XX
PF 05-JUL-1996; 96US-0675816.
XX
PR 05-JUL-1996; 96US-0675816.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Coughlan SJ, Winfrey RJ;
XX
DR WPI; 2001-122335/13.
DR N-PSDB; AAF29741, AAF29742.
XX
PT New nucleic acid molecules encoding a calcium binding chaperone protein

PT in endoplasmic reticulum, calreticulin, and calreticulin promoter
PT sequences, useful for producing foreign gene products in plant cells
XX
PS Claim 1; Fig 3; 45pp; English.
XX
CC The present invention provides the protein and coding sequences for the
CC castor bean calreticulin protein and the calreticulin promoter sequence.
CC In addition, the castor bean calnexin protein, coding sequence and
CC promoter are also described. Calreticulin and calnexin are calcium
CC binding proteins found in the endoplasmic reticulum (er). The
CC calreticulin promoter sequence can be used in vectors to promote the
CC expression of foreign genes, particularly resistance genes, in plant
CC cells.
XX Sequence 415 AA;

Query Match 54.3%; Score 527; DB 22; Length 415;
Best Local Similarity 55.3%; Pred. No. 1e-49;
Matches 99; Conservative 31; Mismatches 43; Indels 6; Gaps 3;
QY 4 VYKEQFLDGDGWTSRWIESKHKSD---FGKFLSSGKFGYGDDEKGLQTSQDAREVAL 60
Db 22 vfeerf--edgwenrvwksdwkdkentagewnytsgkwngd-pndkgigtcsedyrfyai 78
QY 61 SASFEPFNSNKGOTLVVQFTVKHEQNTDCGGYVKLFPNSLDQTMHGDSEYNTMGPDIC 120
Db 79 saefefsnkdktlvfqfsvkheqidecggvymkllsstdqkkfggtpysimgpdc 138
QY 121 GPGTKKHVHFYFNKGNVLINKDIRCKDDEFTHLTYLIVRPONTYEVKIDNSQVESGSL 179
Db 139 gystkvhailnyndtnhlikkevpcetqlchvylvirpdatsillidnvektgsl 197

RESULT 11
AAB66343
ID AAB66343 standard; Protein; 415 AA.
XX
AC AAB66343;
XX
DT 05-APR-2001 (first entry)
XX
DE Castor bean calreticulin.
XX
KW Castor bean; calreticulin; calcium binding; er; endoplasmic reticulum;
KW calnexin; promoter; resistance.
XX
OS Ricinus communis.
XX
PN US6171864-B1.
XX
PD 09-JAN-2001.
XX
PF 05-JUL-1996; 96US-0675816.
XX
PR 05-JUL-1996; 96US-0675816.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Coughlan SJ, Winfrey RJ;
XX
DR WPI; 2001-122335/13.
DR N-PSDB; AAF29755.
XX
PT New nucleic acid molecules encoding a calcium binding chaperone protein
PT in endoplasmic reticulum, calreticulin, and calreticulin promoter
PT sequences, useful for producing foreign gene products in plant cells
XX
PS Disclosure; Fig 1B; 45pp; English.

XX The present invention provides the protein and coding sequences for the
XX castor bean calreticulin protein and the calreticulin promoter sequence.
XX In addition, the castor bean calnexin protein, coding sequence and

CC promoter are also described. Calreticulin and calnexin are calcium
CC binding proteins found in the endoplasmic reticulum (er). The
CC calreticulin promoter sequence can be used in vectors to promote the
CC expression of foreign genes, particularly resistance genes, in plant
XX cells.

SQ Sequence 415 AA;

Query Match 54.3%; Score 527; DB 22; Length 415;
Best Local Similarity 55.3%; Pred. No. 1e-49;
Matches 99; Conservative 31; Mismatches 43; Indels 6; Gaps 3;

OY 4 VYFKEFLDGDGWTSMWIESKKSD---FGKVLSSGKFGYGDDEKDKGLQTSODARFYAL 60

Db 22 vffeerf--edgwenrwksdwkdkdentagewnytsqkwnqd-pndkgigtsey-fyal 78

OY 61 SASFEFSSKGGTLLVQFVFKHEQNTDCGGYVVKLPNSLDQTMHGDSYNTMFGPDIC 120

Db 79 saefpfsnkdktlvfqsvkheqkdcggymkllssstdqkfggdtptyslmfpgdic 138

OY 121 GPOTKKVHFYFNKGNVLINKDIRCKDDEFTHLVTLVIRPDNTYEVKIDNSOVESGSL 179

Db 139 gystkkvhailnyndnhikkevpeetdqthvylvirpdatysilldnvektqtsl 197

RESULT 12

AG24608

ID AAG24608 standard; Protein; 421 AA.

AC AAG24608;

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 26350.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

OS Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126264.

XX 29-MAR-1999; 99US-0126785.

XX 01-APR-1999; 99US-0127462.

XX 06-APR-1999; 99US-0128234.

XX 08-APR-1999; 99US-0128714.

XX 16-APR-1999; 99US-0129845.

XX 19-APR-1999; 99US-0130077.

XX 21-APR-1999; 99US-0130449.

XX 23-APR-1999; 99US-0130510.

XX 28-APR-1999; 99US-0130891.

XX 30-APR-1999; 99US-0131449.

XX 04-MAY-1999; 99US-0132407.

XX 05-MAY-1999; 99US-0132484.

XX 06-MAY-1999; 99US-0132485.

XX 07-MAY-1999; 99US-0132486.

XX 11-MAY-1999; 99US-0132487.

XX 14-MAY-1999; 99US-0132486.

XX 14-MAY-1999; 99US-0134218.

XX 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134221.

PR 14-MAY-1999; 99US-0134370.

PR 18-MAY-1999; 99US-0134768.

PR 19-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.

PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.

PR 01-JUN-1999; 99US-0137222.

PR 03-JUN-1999; 99US-0137528.

PR 04-JUN-1999; 99US-0137502.

PR 07-JUN-1999; 99US-0137724.

PR 08-JUN-1999; 99US-0138094.

PR 10-JUN-1999; 99US-0138540.

PR 10-JUN-1999; 99US-0138847.

PR 14-JUN-1999; 99US-0139119.

PR 16-JUN-1999; 99US-0139452.

PR 16-JUN-1999; 99US-0139453.

PR 17-JUN-1999; 99US-0139492.

PR 18-JUN-1999; 99US-0139454.

PR 18-JUN-1999; 99US-0139455.

PR 18-JUN-1999; 99US-0139456.

PR 18-JUN-1999; 99US-0139457.

PR 18-JUN-1999; 99US-0139458.

PR 18-JUN-1999; 99US-0139459.

PR 18-JUN-1999; 99US-0139460.

PR 18-JUN-1999; 99US-0139461.

PR 18-JUN-1999; 99US-0139462.

PR 18-JUN-1999; 99US-0139463.

PR 18-JUN-1999; 99US-0139750.

PR 21-JUN-1999; 99US-0139763.

PR 21-JUN-1999; 99US-0139817.

PR 22-JUN-1999; 99US-0139899.

PR 23-JUN-1999; 99US-0140353.

PR 23-JUN-1999; 99US-0140354.

PR 24-JUN-1999; 99US-0140695.

PR 28-JUN-1999; 99US-0140823.

PR 29-JUN-1999; 99US-0140991.

PR 30-JUN-1999; 99US-0141287.

PR 01-JUL-1999; 99US-0141842.

PR 01-JUL-1999; 99US-0142154.

PR 02-JUL-1999; 99US-0142055.

PR 06-JUL-1999; 99US-0142390.

PR 08-JUL-1999; 99US-0142803.

PR 09-JUL-1999; 99US-0142920.

PR 12-JUL-1999; 99US-0142977.

PR 13-JUL-1999; 99US-0143542.

PR 14-JUL-1999; 99US-0143624.

PR 15-JUL-1999; 99US-0144005.

PR 16-JUL-1999; 99US-0144085.

PR 16-JUL-1999; 99US-0144086.

PR 19-JUL-1999; 99US-0144325.

PR 19-JUL-1999; 99US-0144331.

PR 19-JUL-1999; 99US-0144332.

PR 19-JUL-1999; 99US-0144333.

PR 19-JUL-1999; 99US-0144334.

PR 19-JUL-1999; 99US-0144335.

PR 20-JUL-1999; 99US-0144352.

PR 20-JUL-1999; 99US-0144632.

PR 20-JUL-1999; 99US-0144884.

PR 21-JUL-1999; 99US-0144814.

PR 21-JUL-1999; 99US-0145086.

PR 21-JUL-1999; 99US-0145088.

PR 22-JUL-1999; 99US-0145085.

PR 22-JUL-1999; 99US-0145087.

PR 22-JUL-1999; 99US-0145089.

PR 22-JUL-1999; 99US-0145192.

PR 23-JUL-1999; 99US-0145145.

PR 23-JUL-1999; 99US-0145218.

PR 23-JUL-1999; 99US-0145224.

PR 26-JUL-1999; 99US-0145276.

PR 14-MAY-1999; 99US-0134219.
 PR 14-MAY-1999; 99US-0134221.
 PR 14-MAY-1999; 99US-0134370.
 PR 18-MAY-1999; 99US-0134768.
 PR 19-MAY-1999; 99US-0134941.
 PR 20-MAY-1999; 99US-0135124.
 PR 21-MAY-1999; 99US-0135353.
 PR 24-MAY-1999; 99US-0135629.
 PR 25-MAY-1999; 99US-0136021.
 PR 27-MAY-1999; 99US-0136392.
 PR 28-MAY-1999; 99US-0136782.
 PR 01-JUN-1999; 99US-0137222.
 PR 03-JUN-1999; 99US-0137528.
 PR 04-JUN-1999; 99US-0137502.
 PR 07-JUN-1999; 99US-0137724.
 PR 08-JUN-1999; 99US-0138094.
 PR 10-JUN-1999; 99US-0138540.
 PR 10-JUN-1999; 99US-0138847.
 PR 14-JUN-1999; 99US-0139119.
 PR 16-JUN-1999; 99US-0139452.
 PR 16-JUN-1999; 99US-0139453.
 PR 17-JUN-1999; 99US-0139454.
 PR 18-JUN-1999; 99US-0139455.
 PR 18-JUN-1999; 99US-0139456.
 PR 18-JUN-1999; 99US-0139457.
 PR 18-JUN-1999; 99US-0139458.
 PR 18-JUN-1999; 99US-0139459.
 PR 18-JUN-1999; 99US-0139460.
 PR 18-JUN-1999; 99US-0139461.
 PR 18-JUN-1999; 99US-0139462.
 PR 18-JUN-1999; 99US-0139463.
 PR 18-JUN-1999; 99US-0139750.
 PR 18-JUN-1999; 99US-0139763.
 PR 21-JUN-1999; 99US-0139817.
 PR 22-JUN-1999; 99US-0139899.
 PR 23-JUN-1999; 99US-0140353.
 PR 23-JUN-1999; 99US-0140354.
 PR 24-JUN-1999; 99US-0140695.
 PR 28-JUN-1999; 99US-0140823.
 PR 29-JUN-1999; 99US-0140991.
 PR 30-JUN-1999; 99US-0141287.
 PR 01-JUL-1999; 99US-0141842.
 PR 01-JUL-1999; 99US-0142154.
 PR 02-JUL-1999; 99US-0142055.
 PR 02-JUL-1999; 99US-0142390.
 PR 06-JUL-1999; 99US-0142803.
 PR 08-JUL-1999; 99US-0142920.
 PR 09-JUL-1999; 99US-0142977.
 PR 12-JUL-1999; 99US-0143542.
 PR 13-JUL-1999; 99US-0143624.
 PR 15-JUL-1999; 99US-0144005.
 PR 16-JUL-1999; 99US-0144085.
 PR 16-JUL-1999; 99US-0144086.
 PR 19-JUL-1999; 99US-0144325.
 PR 19-JUL-1999; 99US-0144331.
 PR 19-JUL-1999; 99US-0144332.
 PR 19-JUL-1999; 99US-0144333.
 PR 19-JUL-1999; 99US-0144334.
 PR 19-JUL-1999; 99US-0144335.
 PR 20-JUL-1999; 99US-0144352.
 PR 20-JUL-1999; 99US-0144632.
 PR 20-JUL-1999; 99US-0144884.
 PR 21-JUL-1999; 99US-0144814.
 PR 21-JUL-1999; 99US-0145086.
 PR 21-JUL-1999; 99US-0145088.
 PR 22-JUL-1999; 99US-0145085.
 PR 22-JUL-1999; 99US-0145087.
 PR 22-JUL-1999; 99US-0145089.
 PR 22-JUL-1999; 99US-0145192.
 PR 23-JUL-1999; 99US-0145145.
 PR 23-JUL-1999; 99US-0145218.
 PR 23-JUL-1999; 99US-0145224.

PR 26-JUL-1999; 99US-0145276.
 PR 27-JUL-1999; 99US-0145913.
 PR 27-JUL-1999; 99US-0145918.
 PR 27-JUL-1999; 99US-0145919.
 PR 28-JUL-1999; 99US-0145951.
 PR 02-AUG-1999; 99US-0146386.
 PR 02-AUG-1999; 99US-0146388.
 PR 02-AUG-1999; 99US-0146389.
 PR 03-AUG-1999; 99US-0147038.
 PR 04-AUG-1999; 99US-0147204.
 PR 04-AUG-1999; 99US-0147302.
 PR 05-AUG-1999; 99US-0147192.
 PR 05-AUG-1999; 99US-0147260.
 PR 06-AUG-1999; 99US-0147303.
 PR 06-AUG-1999; 99US-0147416.
 PR 09-AUG-1999; 99US-0147493.
 PR 09-AUG-1999; 99US-0147935.
 PR 10-AUG-1999; 99US-0148171.
 PR 11-AUG-1999; 99US-0148319.
 PR 12-AUG-1999; 99US-0148341.
 PR 13-AUG-1999; 99US-0148565.
 PR 13-AUG-1999; 99US-0148684.
 PR 16-AUG-1999; 99US-0149368.
 PR 17-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149722.
 PR 20-AUG-1999; 99US-0149723.
 PR 20-AUG-1999; 99US-0149929.
 PR 23-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
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XX DT 18-OCT-2000 (first entry)

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ALIGNMENTS

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; APPLICANT: Coughlan, Sean J.
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND US
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 701 Fifth Ave. Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
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; FILING DATE: 05-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: NO. 6171864tenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 750027.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206-622-4900
; TELEFAX: (206)-682-6031
; INFORMATION FOR SEQ ID NO: 2:
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; LENGTH: 415 amino acids
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; TOPOLOGY: linear
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US-08-675-816-2

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; APPLICANT: Thomas, David Y.
; APPLICANT: Wada, Ikuo
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; TITLE OF INVENTION: PROTEIN TRAFFICKING DISORDERS AND INCREASING SECRETORY
; TITLE OF INVENTION: PROTEIN PRODUCTION
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; CITY: Seattle
; STATE: Washington
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; ZIP: 98104-7092
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/296.362
; FILING DATE: 25-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deehr, Manya S.
; REGISTRATION NUMBER: 37,120
; REFERENCE/DOCKET NUMBER: 690066.401C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 622-6031
; TELE: 3723836
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 593 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-296-362-2

Query Match 29.9%; Score 290; DB 1; Length 593;
Best Local Similarity 38.1%; Pred. No. 2.1e-24;
Matches 77; Conservative 26; Mismatches 65; Indels 34; Gaps 9;

QY 4 VYFKEQFLDGCWTSRWIESKHKSD-----FGKVLSSGKFGYGDREK-----DKGLQTS 52
Db 70 VYFASG--DRTLSGWLISLAKAKDQTDDEIAKY---DGKWEVDENKTKLPDGLVLM 124
QY 53 QDAREYALSASF-EFFSNKGOTLVVQFTVKHEQNDICGGYVYKFLFPN-----SLDQTDHMG 107
Db 125 SRAKHHAISAKLNKPFQTKPLVQYEVFNQIECGGAYVYKLLSKTPELNLDQ--PHD 182
QY 108 DSEYNTMFGPDICGPGTKVHVIFNFKGNVLYNKDICKDDFTHLYTLVIRPNTYEVKIDNSQ 157
Db 183 KPTPTIMFGPDICGGE-DYKLFHIFRHKPKTGTYVEEKHAKRPDADLKTYFTOKKTHLYTL 241
QY 158 IVRPONTYEVKIDNSQVSGSL 179
Db 242 ILNPNSEFELVDQSIIVNSGNL 263
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RESULT 3
US-08-675-816-6
; Sequence 6, Application US/08675816
; Patent No. 6171864
; GENERAL INFORMATION:
; APPLICANT: Coughlan, Sean J.
; APPLICANT: Winfrey, Ron J.
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND US
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 701 Fifth Ave. Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675.816
; FILING DATE: 05-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6171864tenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 750027.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206-622-4900
; TELEFAX: (206)-682-6031
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 542 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-675-816-6

Query Match 23.4%; Score 227.5; DB 4; Length 542;
Best Local Similarity 36.0%; Pred. No. 2.2e-17;
Matches 64; Conservative 24; Mismatches 73; Indels 17; Gaps 10;

QY 6 FKEQFLDGCWTSRWIESKHKSDFGKVLSSGKFGYGDREKGLQTSQDAREYALSASF- 64
Db 35 FYESEF--EDSFEGRWTLA-KDDY-KGEWKHAKSEGHDE--YGLLVSEKARKYAIYKELD 88
QY 65 EPFSNKGOTLVVQFTVKHEQNDICGGYVYK-LFPNSLDQT--DMHGDSEYNIMFGPDICG 121
Db 89 EATLKDGTIVLQFETRFQNGIECGGAYVYKLYRPOEAGWTPKDFDNDSPYSIMFGPDICG 148
QY 122 PGTKVHVIFNFKG--KNVLYNKDIR----CKDDEFTHTLYTLVIRPNTYEVKIDNSQ 173
Db 149 -ATNKVHFILKHKPKSGYIEHHLKYPSPVSDKLTHVYTAILKPDNELRLIVDGE 205

RESULT 4
US-09-181-706-8
; Sequence 8, Application US/09181706
; Patent No. 6130068
; GENERAL INFORMATION:
; APPLICANT: Melanie K. Spriggs, Michael R. Comeau,
; APPLICANT: Robert F. Dubose, Richard S. Johnson
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle
```

```

RESULT      6
US-09-459-066-8
; Sequence 8, Application US/09459066
; Patent No. 6187909
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/Windows 95
; SOFTWARE: Word for Windows 95, 7.0a

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;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/459,066
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/958,598
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Henry, Janis C
;; REGISTRATION NUMBER: 34,347
;; REFERENCE/DOCKET NUMBER: 2631
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206)470-4189
;; TELEFAX: (206)233-0644
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 660 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-459-066-8

Query Match 9.2%; Score 89; DB 4; Length 660;
Best Local Similarity 20.6%; Pred. No. 0.14;
Matches 41; Conservative 25; Mismatches 91; Indels 42; Gaps 6;
QY 5 YFKQFLDGGQWTSRWTSKHKSDGKFLVLS---SGKFGYGDDEKDKGLQTSQDARFYALS 61
DB 448 YIAQCLNDEGSPSS-LSSHNWSTFLKVELCDIDGRSQRQIIHSKAIKATNDNTILYVFF 506
QY 62 ASFPFSGKQGLVQVFTVXHEQVNDGCGGVYKLFNPSLDQTDHMGDSEYNIMFGPDICG 121
DB 507 DS--PYSKALCTYSMAIKHSFSTSLGKGVTKQLPSP-----APGICL 548
QY 122 PGTKV-HVTFN-----YKKNVLINKDICKDDETHLYTLVRP 161
DB 549 PAGVVPHTTFTIEQYNELDDIITKPLSQPIFGPSGVKWFIDKEKENHREYRIYFIKE 608
QY 162 DNTVEVKIDNSQVESGSL 180
DB 609 NTIYFDTKSKQTRSAQVD 627

RESULT 7
US-08-245-511-48
; Sequence 48, Application US/08245511
; Patent No. 5928900
; GENERAL INFORMATION:
; APPLICANT: Masure, H Robert
; APPLICANT: Pearce, Barbara J
; APPLICANT: Tuomanen, Elaine
; TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND
; TITLE OF INVENTION: ACCELLULAR VACCINES BASED THEREON
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/245,511
; FILING DATE: 18-MAY-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/116,541

;; FILING DATE: 01-SEP-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jackson Esq., David A.
;; REGISTRATION NUMBER: 26,742
;; REFERENCE/DOCKET NUMBER: 600-1-069 CIP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201 487-5800
;; TELEFAX: 201 343-1684
;; TELEX: 133521
;; INFORMATION FOR SEQ ID NO: 48:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 642 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Streptococcus pneumoniae
;; IMMEDIATE SOURCE:
;; CLONE: am1A
;; FEATURE:
;; OTHER INFORMATION: NOTE: the reference contains a
;; OTHER INFORMATION: sequence error; the correct sequence shown below is obtain
;; OTHER INFORMATION: from GENBANK
;; PUBLICATION INFORMATION:
;; AUTHORS: Allouing, et al.
;; JOURNAL: Mol. Microbiol.
;; VOLUME: 4
;; PAGES: 633-644
;; DATE: 1990
US-08-245-511-48

Query Match 8.0%; Score 77.5; DB 2; Length 642;
Best Local Similarity 21.2%; Pred. No. 2.6;
Matches 42; Conservative 20; Mismatches 81; Indels 55; Gaps 8;
QY 16 WTSP-----W-----TESKHSDFGKFLVLSGKFGYGDDEKDKGLQTSQDARFYALSASF 64
DB 164 WNSKLTYSIFWPLNEEFETSKGSDFAKPTDPTSLLYNGPFLKGLTAKSSVEF-----VKN 219
QY 65 EPPSNKGQTLVQVFTVKH-----EQNIDCGG-GYVKLFNPSLDQTDHMGDSEY 111
DB 220 EGYWDKENVHLDITNLAYIDGSDQESLERNFSTGAYSARLYPTSSNYSKVAEYKDIY 279
QY 112 NIMFGPDICGPTKKVHVIFNYKG-----KNVLINKDIR----- 145
DB 280 YTQSGSGIAGLGVNIDRQSYNTSKTTDSEKVAATKALLNKDFRQALNFALDRSAYSQAI 339
QY 146 -CKDDETHLYTLVRPD 162
DB 340 NGKDGALAVRNLFVKPD 357
RESULT 8
US-08-600-993A-48
; Sequence 48, Application US/08600993A
; Patent No. 5981229
; GENERAL INFORMATION:
; APPLICANT: Masure, H Robert
; APPLICANT: Pearce, Barbara J
; APPLICANT: Tuomanen, Elaine
; TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND
; TITLE OF INVENTION: ACCELLULAR VACCINES BASED THEREON
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601


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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991.408
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/034,471
; FILING DATE: 02-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: ATG-50038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-991-408-4

Query Match 7.7%; Score 75; DB 3; Length 591;
Best Local Similarity 31.4%; Pred. No. 4.5;
Matches 33; Conservative 15; Mismatches 39; Indels 18; Gaps 7;

QY 68 SNKGQTLVVQF--TVKHEQNIDCGGKVLFPNSLDQTMHGDSEYNIMFGPDICPGG-TK 125
DB 501 SRGSRLELSFQTFEVEEADCGYDVELF-DGLDSTAV-GLGRF-----CGSGPPE 550

QY 126 KVHVIFNYKGNVLI--NKDIRCKDDETHLYTLIVRPDNTYEVK 168
DB 551 EIYSI-----GDSVLHFHTDDTINKKGFHRYKSIRYPTDTHTKK 591

RESULT 11
US-08-866-650-5
; Sequence 5, Application US/08866650
; Patent No. 5939321
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Daniel S
; APPLICANT: Takahara, Kazuhiko
; APPLICANT: Hoffman, Guy G
; TITLE OF INVENTION: Mammalian Tolloid-Like Protein
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/866,650
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/866,650
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berson, Bennett J
; REGISTRATION NUMBER: 37094
; REFERENCE/DOCKET NUMBER: 960296.93839
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1013 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-828-000-3.ra1
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;
; LENGTH: 1013 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-866-650-5

Query Match 7.7%; Score 75; DB 2; Length 1013;
Best Local Similarity 31.4%; Pred. No. 9.7;
Matches 33; Conservative 15; Mismatches 39; Indels 18; Gaps 7;

QY 68 SNKGQTLVVQF--TVKHEQNIDCGGKVLFPNSLDQTMHGDSEYNIMFGPDICPGG-TK 125
DB 923 SRGSRLELSFQTFEVEEADCGYDVELF-DGLDSTAV-GLGRF-----CGSGPPE 972

QY 126 KVHVIFNYKGNVLI--NKDIRCKDDETHLYTLIVRPDNTYEVK 168
DB 973 EIYSI-----GDSVLHFHTDDTINKKGFHRYKSIRYPTDTHTKK 1013

RESULT 12
US-09-021-287-5
; Sequence 5, Application US/09021287
; Patent No. 5981717
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Daniel S
; APPLICANT: Takahara, Kazuhiko
; APPLICANT: Hoffman, Guy G
; TITLE OF INVENTION: Mammalian Tolloid-Like Protein
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/021,287
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/866,650
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berson, Bennett J
; REGISTRATION NUMBER: 37094
; REFERENCE/DOCKET NUMBER: 960296.93839
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1013 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-021-287-5

Query Match 7.7%; Score 75; DB 2; Length 1013;
Best Local Similarity 31.4%; Pred. No. 9.7;
Matches 33; Conservative 15; Mismatches 39; Indels 18; Gaps 7;

QY 68 SNKGQTLVVQF--TVKHEQNIDCGGKVLFPNSLDQTMHGDSEYNIMFGPDICPGG-TK 125
DB 923 SRGSRLELSFQTFEVEEADCGYDVELF-DGLDSTAV-GLGRF-----CGSGPPE 972
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QY 126 KHVIFNYKGNVLI--NKDIRCKDDETHLYTLVLRPONTYEVK 168
Db 973 EIYSI-----GDSVLIHFHTDDTINKKGFIHYKSIKIRYPTDTHTKK 1013

RESULT 13

US-08-991-408-2
; Sequence 2, Application US/08991408
; Patent No. 6008017
; GENERAL INFORMATION:
; APPLICANT: ARLETH, ANTHONY J.
; APPLICANT: WILLETTE, ROBERT N.
; APPLICANT: ELSHOURBAGY, NABIL A.
; APPLICANT: LI, XIAOFONG
; TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,408
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/034,471
; FILING DATE: 02-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: ATG-50038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1013 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-991-408-2

Query Match 7.7%; Score 75; DB 3; Length 1013;
Best Local Similarity 31.4%; Pred. No. 9.7;
Matches 33; Conservative 15; Mismatches 39; Indels 18; Gaps 7;

QY 68 SNKGQTLVVOF-TVKHEQNIDCGGVYKLPNLSLDQTDMDHGDSEYNIMFGPDTCGPG-TK 125
Db 923 SERGSRLELSFQFVEEADCGYDYVELF-DGLDSTAV-GLGRF-----CGSGPPE 972
QY 126 KHVIFNYKGNVLI--NKDIRCKDDETHLYTLVLRPONTYEVK 168
Db 973 EIYSI-----GDSVLIHFHTDDTINKKGFIHYKSIKIRYPTDTHTKK 1013

RESULT 14

US-09-240-473-5
; Sequence 5, Application US/09240473
; Patent No. 6297011
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Daniel S

; APPLICANT: Takahara, Kazuhiko
; APPLICANT: Hoffman, Guy G
; TITLE OF INVENTION: Mammalian Tolloid-Like Protein
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/240,473
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berson, Bennett J
; REGISTRATION NUMBER: 37094
; REFERENCE/DOCKET NUMBER: 960296.93839
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1013 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-240-473-5

Query Match 7.7%; Score 75; DB 4; Length 1013;
Best Local Similarity 31.4%; Pred. No. 9.7;
Matches 33; Conservative 15; Mismatches 39; Indels 18; Gaps 7;

QY 68 SNKGQTLVVOF-TVKHEQNIDCGGVYKLPNLSLDQTDMDHGDSEYNIMFGPDTCGPG-TK 125
Db 923 SERGSRLELSFQFVEEADCGYDYVELF-DGLDSTAV-GLGRF-----CGSGPPE 972
QY 126 KHVIFNYKGNVLI--NKDIRCKDDETHLYTLVLRPONTYEVK 168
Db 973 EIYSI-----GDSVLIHFHTDDTINKKGFIHYKSIKIRYPTDTHTKK 1013

RESULT 15

US-08-231-193A-56
; Sequence 56, Application US/08231193A
; Patent No. 5849895
; GENERAL INFORMATION:
; APPLICANT: Daggett, Lorrie P.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lu, Chin-Chun

; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
; TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/231.193A
; FILING DATE: 20-APR-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/052,459
; FILING DATE: 20-APR-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1484 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-231-193A-56

Query Match
Best Local Similarity 7.5%; Score 72.5; DB 2; Length 1484;
Matches 23; Conservative 13; Mismatches 28; Indels 19; Gaps 4;

QY 45 KDKG--LQTSQDARYALASAPFSPNKGQTLVQFTVKHEQIDCGGYV---KLFPS 99
    ||| : | : | : | : | : | : | : | : | : | : | : | : | :
DB 1325 KDKGRFMDGSPYAHMFENSAGESTEFANKSSVP---TAGHHHHNNPGGGYMLSKSLYPD 1381
    ||| : | : | : | : | : | : | : | : | : | : | : | : | :

QY 100 L-----DQTDHMGDSY 111
    : | : | : | : | : | : | : | : | : | : | : | : | :
DB 1382 VTQNPFIPTFGDDQCLLHGSKSY 1404
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Search completed: January 9, 2002, 14:59:42
Job time: 69 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 9, 2002, 14:58:53 ; Search time 43.73 Seconds
(without alignments)
313.547 Million cell updates/sec

Title: US-09-828-000-3

Perfect score: 971
Sequence: 1 EPAVYFKEQFLDGDGWTSRW.....PDNTYEVKIDNSQVESGSLE 180

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	971	100.0	417	1 A37047	calreticulin precu
2	933	96.1	416	2 JH0819	calreticulin precu
3	931	95.9	418	1 A34154	calreticulin precu
4	930	95.8	400	2 S43376	calreticulin, brai
5	930	95.8	416	1 S06763	calreticulin precu
6	835	86.0	411	2 S29129	calreticulin precu
7	804	82.8	405	1 JH0795	calreticulin precu
8	797	82.1	384	2 S29130	calreticulin (clon
9	796	82.0	419	2 S71343	calreticulin precu
10	699	72.0	406	2 A56637	calreticulin homol
11	619.5	63.8	395	2 S25851	calreticulin precu
12	542.5	55.9	336	2 A32507	41K larval antigen
13	539	55.5	412	2 T05703	calreticulin - bar
14	539	55.5	415	2 T05705	calreticulin - bar
15	536	55.2	421	2 S58170	calreticulin precu
16	531	54.7	416	2 T14554	calreticulin - bee
17	527	54.3	415	2 T10172	calreticulin - cas
18	522.5	53.8	421	2 S36799	calreticulin precu
19	522	53.8	416	2 T16968	calreticulin call
20	517	53.2	389	2 T03691	calreticulin - com
21	512	52.7	425	2 C96605	calreticulin (crtl
22	510	52.5	444	2 H86224	hypothetical prot
23	496	51.1	393	1 A48573	calreticulin autoa
24	347	35.7	422	2 T07841	probable calreticu
25	293	30.2	591	2 B54354	calnexin precursor
26	290	29.9	591	2 C54354	calnexin precursor
27	290	29.9	592	2 I53260	calnexin - human
28	290	29.9	593	1 A37273	calnexin precursor
29	288	29.7	592	2 A46673	calnexin precursor

30	270	27.8	611	2 A53418	calmeglin precursor
31	262	27.0	622	2 S71342	calnexin precursor
32	253.5	26.1	560	2 S56142	calcium-binding pr
33	252	26.0	611	2 A54086	calnexin-t - mouse
34	248	25.5	582	2 A46637	calnexin homolog S
35	244	25.1	619	2 S40938	hypothetical prote
36	238.5	24.6	530	2 JN0597	calnexin-like prot
37	232	23.9	546	2 T08415	calnexin - soybean
38	215.5	22.2	540	2 T10892	probable calnexin
39	200.5	20.6	532	2 T49873	calnexin homolog -
40	157	16.2	29	2 E33208	calreticulin, uter
41	145	14.9	29	2 C33208	calreticulin, slow
42	144	14.8	29	2 D33208	calreticulin, brai
43	133.5	13.7	502	2 S29347	calnexin homolog Y
44	129	13.3	297	2 S70552	calnexin homolog C
45	124.5	12.8	428	2 T03251	calnexin - maize (

ALIGNMENTS

RESULT 1
A37047
calreticulin precursor - human
N:Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K integrin-binding pr
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Feb-2000
C:Accession: A42330; A37047; A46452; A28812; A40346; S11475; T45075
R:McCaulliffe, D.P.; Yang, Y.S.; Wilson, J.; Sontheimer, R.D.; Capra, J.D.
J. Biol. Chem. 267, 2557-2562, 1992
A:Title: The 5'-flanking region of the human calreticulin gene shares homology with t
A:Reference number: A42330; MUID:92129342
A:Accession: A42330
A:Molecule type: DNA
A:Residues: 1-417 <MC2>
A:Note: sequence extracted from NCBI backbone (NCBIN:78537, NCBI:78536)
R:McCaulliffe, D.P.; Lux, F.A.; Lieu, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachin
J. Clin. Invest. 85, 1379-1391, 1990
A:Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/
A:Reference number: A37047; MUID:90237213
A:Accession: A37047
A:Molecule type: mRNA
A:Residues: 1-417 <MCC>
A:Cross-references: GB:M32294; NID:G37486; PIDN:AAA36582.1; PID:G337487
R:Rothead, L.A.; Haselby, J.A.; Meilof, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.
J. Immunol. 147, 3031-3039, 1991
A:Title: Characterization of the autoantigen calreticulin.
A:Reference number: A46452; MUID:92013129
A:Accession: A46452
A:Molecule type: mRNA
A:Residues: 1-417 <ROK>
A:Cross-references: GB:M84739; NID:G179881; PIDN:AAA51916.1; PID:G179882
R:Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sontheimer, R.D.
J. Clin. Invest. 82, 96-101, 1988
A:Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence
A:Reference number: A28812; MUID:88273610
A:Accession: A28812
A:Molecule type: protein
A:Residues: 18-41 <LIE>
A:Note: 18-Ala was also found
R:Dupuis, M.; Schaefer, E.; Krause, K.H.; Tschopp, J.
J. Exp. Med. 177, 1-7, 1993
A:Title: The calcium-binding protein calreticulin is a major constituent of lytic gra
A:Reference number: PH1525; MUID:93115648
A:Accession: PH1525
A:Molecule type: protein
A:Residues: 18-27 <DUP>
A:Experimental source: LAK cell
R:Roizani, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.
Biochemistry 30, 9859-9866, 1991
A:Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (c

A:Reference number: A40346; MUID:92002034
A:Accession: A40346
A:Molecule type: protein
A:Residues: 18-34, 'R' <RO>
R:Krause, K.H.; Simmerman, H.K.B.; Jones, L.R.; Campbell, K.P.
Biochem. J. 270, 545-548, 1990
A:Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that co-purifies with the Golgi apparatus
A:Reference number: S11475; MUID:90380058
A:Accession: S11475
A:Molecule type: protein
A:Residues: 18-32 <KRA>
R:Lamerdin, J.; McCready, P.; Stilwagen, S.; Ramirez, M.; Carrano, A.
submitted to the EMBL Data Library, November 1996
A:Description: Characterization by genomic sequence analysis of a gene-rich 111 kb region on chromosome 17p11.2
A:Reference number: 222906
A:Accession: T45075
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-417 <LAM>
A:Cross-references: EMBL:AD000092; PIDN:AA851176.1
A:Experimental source: cell line 5HL2-B; fibroblast
C:Comment: Autoantibodies specific for this protein are found in Sjogren's syndrome and Sjogren's syndrome
C:Genetics:
A:Gene: GDB:CALR
A:Cross-references: GDB:125179; OMIM:109091
A:Map position: 19p13.3-19p13.2
A:Introns: 31/1; 65/1; 133/1; 164/3; 272/3; 320/3; 351/3
A:Note: CRTC
C:Superfamily: calreticulin
C:Keywords: calcium binding; integrin binding
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F:18-417/Product: calreticulin #status predicted <MAT>
F:414-417/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 971; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.3e-80;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPAYFKQFLDGDGWTNRWIESKHSKSDFGKFLVSSGKFGYDGEKDKGLQTSQDARFYAL 60
Db 18 EPAYFKQFLDGDGWTNRWIESKHSKSDFGKFLVSSGKFGYDGEKDKGLQTSQDARFYAL 77

Qy 61 SASPEFFNKGQTLVQVTVKHEQIDCGGVKFLFNSLDQTMHGDSEYNMFPGDIC 120
Db 78 SASPEFFNKGQTLVQVTVKHEQIDCGGVKFLFNSLDQTMHGDSEYNMFPGDIC 137

Qy 121 GPGTKVHVIFNYKGNVLINKDKCKDEFTHTLTVLRPNTVEYKIDNSQVSGSLE 180
Db 138 GPGTKVHVIFNYKGNVLINKDKCKDEFTHTLTVLRPNTVEYKIDNSQVSGSLE 197

RESULT 2
JH0819
calreticulin precursor - rat
N:Alternata names: calcium-binding protein 3
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #revision 20-Aug-1994 #text change 20-Jun-2000
C:Accession: JH0819; A49176; S11205; PC1109; S45036; S04867; S39372; A34473; S13045
R:Nakamura, M.; Moriya, M.; Baba, T.; Michikawa, Y.; Yamamoto, T.; Arai, K.; Okinaga, S.
Exp. Cell Res. 205, 101-110, 1993
A:Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosome
A:Reference number: A49176; MUID:93202172
A:Accession: JH0819
A:Molecule type: mRNA
A:Residues: 1-416 <NAK>
A:Cross-references: GB:D78308; NID:g1089798; PIDN:BA411345.1; PID:g1845572
A:Accession: A49176
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-416 <NA2>
A:Cross-references: GB:D78308; NID:g1089798; PIDN:BA411345.1; PID:g1845572
A:Experimental source: Sprague-Dawley, spermatogenic cells

A:Note: sequence extracted from NCBI backbone (NCBIN:127639, NCBIPI:127643)
R:Murthy, K.K.; Banville, D.; Srikant, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel
Nucleic Acids Res. 18, 4933, 1990
A:Title: Structural homology between the rat calreticulin gene product and the Onchocerca volvulus calreticulin
A:Reference number: S11205; MUID:90370496
A:Accession: S11205
A:Molecule type: mRNA
A:Residues: 1-416 <MUR>
A:Cross-references: EMBL:X53363; NID:955854; PIDN:CAA37446.1; PID:g55855
R:Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.
Biochem. Biophys. Res. Commun. 186, 668-673, 1992
A:Title: Calreticulin is present in the acrosome of spermatids of rat testis.
A:Reference number: PC1109; MUID:92360010
A:Accession: PC1109
A:Molecule type: protein
A:Residues: 18-32 <NAK2>
A:Experimental source: testis, strain Sprague-Dawley
R:Soennichsen, B.; Fuehrle, J.; van Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mies
submitted to the EMBL Data Library, May 1994
A:Description: Retention and retrieval: both mechanisms cooperate to maintain calreticulin in the ER
A:Reference number: S45036
A:Accession: S45036
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-416 <SOE>
A:Cross-references: EMBL:X79327; NID:g488840; PIDN:CAA55890.1; PID:g488841
R:Lone, Y.C.; Bailly, A.; Latruffe, N.
submitted to the EMBL Data Library, December 1988
A:Reference number: S04867
A:Accession: S04867
A:Molecule type: mRNA
A:Residues: 'R', 270-358, 'AAG' <LON>
A:Cross-references: EMBL:X13702; NID:g56055; PIDN:CAA31987.1; PID:g930360
A:Note: the authors designated the protein as D-beta-hydroxybutyrate dehydrogenase
R:Yokoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horiuchi, R.; Kametaki, T.
Biochim. Biophys. Acta 1158, 339-344, 1993
A:Title: Identification of protein disulfide isomerase and calreticulin as autoimmunoantigenic proteins in rat liver vesicles
A:Reference number: S39371; MUID:94072621
A:Accession: S39371
A:Molecule type: protein
A:Residues: 18-23, 'X', 25-32 <YOK>
R:Van, P.N.; Peter, F.; Soelling, H.D.
J. Biol. Chem. 264, 17494-17501, 1989
A:Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes
A:Reference number: A34473; MUID:90008920
A:Accession: A34473
A:Status: preliminary
A:Molecule type: protein
A:Residues: 18-36 <VAN>
R:Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; M
Biochem. J. 271, 473-480, 1990
A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage vesicles
A:Reference number: S13045; MUID:91054414
A:Accession: S13045
A:Molecule type: protein
A:Residues: 18-29 <TRE>
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-416/Product: calreticulin #status experimental <MAT>
F:204-212/Region: nuclear location signal
F:413-416/Region: endoplasmic reticulum retention signal
F:344/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 96.1%; Score 933; DB 2; Length 416;
Best Local Similarity 94.4%; Pred. No. 8.8e-77;
Matches 170; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EPAYFKQFLDGDGWTNRWIESKHSKSDFGKFLVSSGKFGYDGEKDKGLQTSQDARFYAL 60
Db 18 DPATYFKQFLDGDGWTNRWIESKHSKSDFGKFLVSSGKFGYDGEKDKGLQTSQDARFYAL 77

Query Match 55.2%; Score 536; DB 2; Length 421;
Best Local Similarity 56.4%; Pred. No. 6.7e-41;
Matches 101; Conservative 31; Mismatches 41; Indels 6; Gaps 3;
QY 4 VYFKEQFLDGDGWTSRWIESKHSD--FGKFVLSGKFGYDDEKDKGLOTSODAREYAL 60
DB 27 VYFQKFP--EDGWESRWVSKENKNDENMAGENHTSGKNGDAE-DKGIOTSEYRFYAI 83
QY 61 SASFEPFSNKGOTLVVQFTVKHEQNIDCGGGYVKLFNSLDQTDHMGDSEYNIMFGPDIC 120
DB 84 SAEPYEPFSNKKDTLVLFQFSVKHEQKLDGCGGYVKLLGGVDVQKKFGGDTSYSIMFGPDIC 143
QY 121 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSL 179
DB 144 GYSTKKVHTILTCKGNHLLIKDVPCETDQLTHTVYTLIIRPDATYSILIDNEEKQTGSI 202

Search completed: January 9, 2002, 15:02:02
Job time: 189 sec

cells.";
RL Biochem. J. 270:545-548(1990).
RN [7]
RP SEQUENCE OF 18-28.
RC TISSUE=Liver;
RX MEDLINE=93162045; PubMed=1286669;
RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
Pascual C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,
Appel R.D., Hughes G.J.;
RT Human liver protein map: a reference database established by
microsequencing and gel comparison.";
RT Electrophoresis 13:992-1001(1992).
RN [8]
RN PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.
RC TISSUE=Keratinocytes;
RX MEDLINE=93162043; PubMed=1286667;
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Cells J.E.,
Vandekerckhove J.;
RT Microsequences of 145 proteins recorded in the two-dimensional gel
protein database of normal human epidermal keratinocytes.";
RL Electrophoresis 13:960-969(1992).
RN [9]
RP SEQUENCE OF 18-26.
RC TISSUE=Colon carcinoma;
RX MEDLINE=97959306; PubMed=9150948;
RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
RT A two-dimensional gel database of human colon carcinoma proteins.";
RL Electrophoresis 18:605-613(1997).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -1- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE THE RO AUTOANTIGEN.
CC
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or send an email to license@isb-sib.ch).
CC
DR EMBL; M84739; AAA51916.1; -;
DR EMBL; M32294; AAA36582.1; -;
DR EMBL; AD000092; AAB51176.1; -;
DR PIR; A37047; A37047.
DR PIR; S11475; S11475.
DR PIR; A42330; A42330.
DR PIR; A46452; A46452.
DR SWISS-2DPAGE; P27797; HUMAN.
DR Aarbus/Ghent-2DPAGE; 9401; IEF.
DR HSC-2DPAGE; P27797; HUMAN.
DR MIM; 109091; -;
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER target.
DR Pfam; PF00262; Calreticulin; 1.
DR PRINTS; PR00636; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER-TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 417 CALRETICULIN.
FT DOMAIN 18 197 P-DOMAIN.
FT DOMAIN 198 308 N-DOMAIN.
FT DOMAIN 309 417 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.

FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 414 417 PREVENT SECRETION FROM ER.
FT CONFLICT 35 35 MISSING (IN REF.3).
SQ SEQUENCE 417 AA; 48141 MW; BC37C3C0F1054FB2 CRC64;

Query Match 100.0%; Score 971; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 4.8e-80;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAVYKQFLDGDGWTSRWIESKHSDFGKFLVSSGKFGYDEEKDKGLQTSODARFYAL 60
DB 18 EPAVYKQFLDGDGWTSRWIESKHSDFGKFLVSSGKFGYDEEKDKGLQTSODARFYAL 77
QY 61 SASFEPFSNKGOTLVVQFTVKHEONIDCGGVYKLPNSLDQTDHMGDSEYNTMFGPDIC 120
DB 78 SASFEPFSNKGOTLVVQFTVKHEONIDCGGVYKLPNSLDQTDHMGDSEYNTMFGPDIC 137
QY 121 GPCTKKVHVIFNYKGNVLIINKDIRCKDDETHLYTLIVRPNTYEVKIDNSQVSGSLE 180
DB 138 GPCTKKVHVIFNYKGNVLIINKDIRCKDDETHLYTLIVRPNTYEVKIDNSQVSGSLE 197

RESULT 2
CRTC_RAT
ID CRTC_RAT STANDARD; PRT; 416 AA.
AC P18418; P10452;
DC 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (BRP60) (CALBP)
DE (CALCIUM-BINDING PROTEIN 3) (CABP3).
GN CALR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain cortex;
RX MEDLINE=90370496; PubMed=2395561;
RA Murthy K.K., Banville D., Srikanth C.B., Carrier F., Bell A.,
Holmes C., Patel Y.C.;
RT "Structural homology between the rat calreticulin gene product and
the Onchocerca volvulus antigen Ral-1.";
RL Nucleic Acids Res. 18:4933-4933(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=93202172; PubMed=8453984;
RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K.,
Okinaga S., Kobayashi T.;
RT "An endoplasmic reticulum protein, calreticulin, is transported into
the acrosome of rat sperm.";
RL Exp. Cell Res. 205:101-110(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RX MEDLINE=95181573; PubMed=7876339;
RA Soennichsen B., Fueflekrug J., van Nguyen P., Diekmann W.,
Robinson D.G., Mieskes G.;
RT "Retention and retrieval: both mechanisms cooperate to maintain
calreticulin in the endoplasmic reticulum.";
RL J. Cell Sci. 107:2705-2717(1994).
RN [4]
RP SEQUENCE OF 270-358 FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;


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Db 121 GPGTKKHVIFNYKGNVINKIRCKDDETHLYTLVRENNTYEVKIDNSQVSGSLE 180
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CRTC_MOUSE
ID CRTC_MOUSE STANDARD; PRT; 416 AA.
AC P14211;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60).
GN CALR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.
RC STRAIN=BALB/C; TISSUE=Liver;
RX MEDLINE=90059955; PubMed=2583110;
RA Smith M.J., Koch G.L.E.;
RT "Multiple zones in the sequence of calreticulin (CRP55, calregulin,
RT HACBP), a major calcium binding ER/SR protein.";
RL EMBO J. 8:3581-3586(1989).
RN [2]
SEQUENCE FROM N.A.
RX MEDLINE=93013037; PubMed=1398135;
RA Mazzarella R.A., Gold P., Cunningham M., Green M.;
RT "Determination of an expressible cDNA clone encoding
RT ERP60/calregulin by the use of a novel nested set method.";
RL Gene 120:217-225(1992).
RN [3]
SEQUENCE OF 18-38.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
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CC -----
DR EMBL; X14926; CAA33053.1; -.
DR EMBL; M92986; AAA37569.1; -.
DR PIR; S06763; S06763.
DR PIR; JC1444; JC1444.
DR SWISS-2DPAGE; P14211; MOUSE.
DR MG; MG1:88252; Calr.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1
FT CHAIN 18 416
FT DOMAIN 18 197

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FT DOMAIN 198 308
FT DOMAIN 309 416
FT DOMAIN 417 416
FT REPEAT 191 202
FT REPEAT 203 210
FT REPEAT 211 221
FT REPEAT 222 238
FT REPEAT 239 255
FT DOMAIN 256 297
FT REPEAT 258 269
FT REPEAT 270 283
FT REPEAT 284 297
FT DOMAIN 300 407
FT DISULFID 308 317
FT SITE 413 416
SQ SEQUENCE 416 AA; 47994 MW; 24C03B00913408D8 CRC64;

Query Match 95.8%; Score 930; DB 1; Length 416;
Best Local Similarity 94.4%; Pred. No. 2.3e-76;
Matches 170; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EPAYVEKEQFLDGDGWTSRWIESKHKSDFGKVLSSGKFGYGDDEKDKGLQTSQDAREVAL 60
Db 18 DPAYFKEQFLDGDGWTNRWVESKHKSDFGKVLSSGKFGYGDDEKDKGLQTSQDAREVAL 77
Qy 61 SASFEFNSKNGQTLVVQFTVKHEQIDCGGKGVKLPNLSLQDTMHGDSYENIMFGPDIC 120
Db 78 SAKTEFNSKNGQTLVVQFTVKHEQIDCGGKGVKLPNLSLQDTMHGDSYENIMFGPDIC 137
Qy 121 GPGTKKHVIFNYKGNVINKIRCKDDETHLYTLVRENNTYEVKIDNSQVSGSLE 180
Db 138 GPGTKKHVIFNYKGNVINKIRCKDDETHLYTLVRENNTYEVKIDNSQVSGSLE 197

RESULT 6
CRTC_MOUSE
ID CRTC_MOUSE STANDARD; PRT; 406 AA.
AC P29413; Q9VHA3;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP).
GN CRC OR CG9429.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=93208374; PubMed=1296819;
RA Smith M.J.;
RT "Nucleotide sequence of a Drosophila melanogaster gene encoding a
RT calreticulin homologue.";
RL DNA Seq. 3:247-250(1992).
RN [2]
SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

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Query Match	68.4%;	Score 564;	DB 1;	Length 388;
Best Local Similarity	67.4%;	Pred. No. 1.7e-52;		
Matches 120;	Conservative 26;	Mismatches 30;	Indels 2;	Gaps 2;
QY	4	VYFKEQFLDGDGWTSSWIESKHKSDFGKFLVSSGKFGYGDGKGLQTSQDARFYALSAS 63		
DB	19	IYFKEDFSB-DWMEKRWTKSKHKDDFGKWEISHGKFGYGDVAKDKGLTKTQDAKFSYGAK 77		
QY	64	FE-PFSNKGQTLVQFTVKHEQNIIDCGGYVKLFNSLDQTMHGDSEYNTMFGPDICGP 122		
DB	78	FDKFSNKGKSLVQFSYKVEHQIDCGGYVKLMSADYNLEDHSGETPYHIMFGPDICGP 137		
QY	123	GTKKVVHVFNYGKKNVLINKDIRCKDDETHLYTLVPRDNTYEVKIDNSQVESGSLE 180		
DB	138	GTKKVVHVFHYKDRNHMKIKDIRCKDDVFTHLYTLVNSDNTYEVQIDGKAESGELE 195		
RESULT	8			
QY	4	VYFKEQFLDGDGWTSSWIESKHKSDFGKFLVSSGKFGYGDGKGLQTSQDARFYALSAS 63		
DB	17	VYFKEEFNDA-SWEKRWQSKHKHDDFGAFKLSAGKFFDVESEDQGIQTSQAKFYISRAK 75		
QY	64	FE-PFSNKGQTLVQFTVKHEQNIIDCGGYVKLFNSLDQTMHGDSEYNTMFGPDICGP 122		
DB	76	FDKFSNKGKTLVQFTVKHEQIDCGGYVKVMRADADLGFHGETPYNMFPGDICGP 135		
QY	123	GTKKVVHVFNYGKKNVLINKDIRCKDDETHLYTLVPRDNTYEVKIDNSQVESGSLE 180		
DB	136	-TRRVHILNYKGENKLKKEITCKSDDELTHLYTLVNSDNTYEVKIDGESAQTSGLE 192		
Query Match	63.8%;	Score 619.5;	DB 1;	Length 395;
Best Local Similarity	63.5%;	Pred. No. 1.7e-48;		
Matches 113;	Conservative 26;	Mismatches 36;	Indels 3;	Gaps 3;
QY	4	VYFKEQFLDGDGWTSSWIESKHKSDFGKFLVSSGKFGYGDGKGLQTSQDARFYALSAS 63		
DB	17	VYFKEEFNDA-SWEKRWQSKHKHDDFGAFKLSAGKFFDVESEDQGIQTSQAKFYISRAK 75		
QY	64	FE-PFSNKGQTLVQFTVKHEQNIIDCGGYVKLFNSLDQTMHGDSEYNTMFGPDICGP 122		
DB	76	FDKFSNKGKTLVQFTVKHEQIDCGGYVKVMRADADLGFHGETPYNMFPGDICGP 135		
QY	123	GTKKVVHVFNYGKKNVLINKDIRCKDDETHLYTLVPRDNTYEVKIDNSQVESGSLE 180		
DB	136	-TRRVHILNYKGENKLKKEITCKSDDELTHLYTLVNSDNTYEVKIDGESAQTSGLE 192		
Query Match	63.8%;	Score 619.5;	DB 1;	Length 395;
Best Local Similarity	63.5%;	Pred. No. 1.7e-48;		
Matches 113;	Conservative 26;	Mismatches 36;	Indels 3;	Gaps 3;
QY	4	VYFKEQFLDGDGWTSSWIESKHKSDFGKFLVSSGKFGYGDGKGLQTSQDARFYALSAS 63		
DB	17	VYFKEEFNDA-SWEKRWQSKHKHDDFGAFKLSAGKFFDVESEDQGIQTSQAKFYISRAK 75		
QY	64	FE-PFSNKGQTLVQFTVKHEQNIIDCGGYVKLFNSLDQTMHGDSEYNTMFGPDICGP 122		
DB	76	FDKFSNKGKTLVQFTVKHEQIDCGGYVKVMRADADLGFHGETPYNMFPGDICGP 135		
QY	123	GTKKVVHVFNYGKKNVLINKDIRCKDDETHLYTLVPRDNTYEVKIDNSQVESGSLE 180		
DB	136	-TRRVHILNYKGENKLKKEITCKSDDELTHLYTLVNSDNTYEVKIDGESAQTSGLE 192		
Query Match	63.8%;	Score 619.5;	DB 1;	Length 395;
Best Local Similarity	63.5%;	Pred. No. 1.7e-48;		
Matches 113;	Conservative 26;	Mismatches 36;	Indels 3;	Gaps 3;
QY	4	VYFKEQFLDGDGWTSSWIESKHKSDFGKFLVSSGKFGYGDGKGLQTSQDARFYALSAS 63		
DB	17	VYFKEEFNDA-SWEKRWQSKHKHDDFGAFKLSAGKFFDVESEDQGIQTSQAKFYISRAK 75		
QY	64	FE-PFSNKGQTLVQFTVKHEQNIIDCGGYVKLFNSLDQTMHGDSEYNTMFGPDICGP 122		
DB	76	FDKFSNKGKTLVQFTVKHEQIDCGGYVKVMRADADLGFHGETPYNMFPGDICGP 135		
QY	123	GTKKVVHVFNYGKKNVLINKDIRCKDDETHLYTLVPRDNTYEVKIDNSQVESGSLE 180		
DB	136	-TRRVHILNYKGENKLKKEITCKSDDELTHLYTLVNSDNTYEVKIDGESAQTSGLE 192		
Query Match	63.8%;	Score 619.5;	DB 1;	Length 395;
Best Local Similarity	63.5%;	Pred. No. 1.7e-48;		
Matches 113;	Conservative 26;	Mismatches 36;	Indels 3;	Gaps 3;
QY	4	VYFKEQFLDGDGWTSSWIESKHKSDFGKFLVSSGKFGYGDGKGLQTSQDARFYALSAS 63		
DB	17	VYFKEEFNDA-SWEKRWQSKHKHDDFGAFKLSAGKFFDVESEDQGIQTSQAKFYISRAK 75		
QY	64	FE-PFSNKGQTLVQFTVKHEQNIIDCGGYVKLFNSLDQTMHGDSEYNTMFGPDICGP 122		
DB	76	FDKFSNKGKTLVQFTVKHEQIDCGGYVKVMRADADLGFHGETPYNMFPGDICGP 135		
QY	123	GTKKVVHVFNYGKKNVLINKDIRCKDDETHLYTLVPRDNTYEVKIDNSQVESGSLE 180		
DB	136	-TRRVHILNYKGENKLKKEITCKSDDELTHLYTLVNSDNTYEVKIDGESAQTSGLE 192		
Query Match	63.8%;	Score 619.5;	DB 1;	Length 395;
Best Local Similarity	63.5%;	Pred. No. 1.7e-48;		
Matches 113;	Conservative 26;	Mismatches 36;	Indels 3;	Gaps 3;
QY	4	VYFKEQFLDGDGWTSSWIESKHKSDFGKFLVSSGKFGYGDGKGLQTSQDARFYALSAS 63		
DB	17	VYFKEEFNDA-SWEKRWQSKHKHDDFGAFKLSAGKFFDVESEDQGIQTSQAKFYISRAK 75		
QY	64	FE-PFSNKGQTLVQFTVKHEQNIIDCGGYVKLFNSLDQTMHGDSEYNTMFGPDICGP 122		
DB	76	FDKFSNKGKTLVQFTVKHEQIDCGGYVKVMRADADLGFHGETPYNMFPGDICGP 135		
QY	123	GTKKVVHVFNYGKKNVLINKDIRCKDDETHLYTLVPRDNTYEVKIDNSQVESGSLE 180		
DB	136	-TRRVHILNYKGENKLKKEITCKSDDELTHLYTLVNSDNTYEVKIDGESAQTSGLE 192		
Query Match	63.8%;	Score 619.5;	DB 1;	Length 395;
Best Local Similarity	63.5%;	Pred. No. 1.7e-48;		
Matches 113;	Conservative 26;	Mismatches 36;	Indels 3;	Gaps 3;
QY	4	VYFKEQFLDGDGWTSSWIESKHKSDFGKFLVSSGKFGYGDGKGLQTSQDARFYALSAS 63		
DB				

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FT REPEAT 211 222 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 246 257 1-4.
FT FT DOMAIN 260 298 3 X 11 AA APPROXIMATE REPEATS.
FT REPEAT 260 270 2-1.
FT REPEAT 274 284 2-2.
FT REPEAT 288 298 2-3.
FT FT DISULFID 105 137 BY SIMILARITY.
FT SITE 421 424 PREVENT SECRETION FROM ER (POTENTIAL).
FT SEQUENCE 424 AA; 48350 MW; BAF273694PBF37 CRC64;

Query Match 55.3%; Score 537; DB 1; Length 424;
Best Local Similarity 57.2%; Pred. No. 4.7e-41;
Matches 103; Conservative 36; Mismatches 33; Indels 8; Gaps

QY 4 VYKPEFLDGDGHTSWIESK-HKSD--FGKPVLSGKFGYGDDEKDKGLQTSQDARFYAL 60
DB 21 VHPKDTF-DND-WESRWVSDMHKDGKGLVHTAGKWFGDENQ-KG1QTSQDARFYAV 77
QY 61 SASPEFSNKGQFLVYQFTVKKHBNIDCGGYYKLPNSLIDQTDHMDGSEYNTIMEGPDIC 120
DB 78 SAFPFSNKGKDLVLYQYVKNQKQVDCGSGYIKLPSKLDQSADFGESEYSIMFGPDVC 137
QY 121 GPCTKKVHVIFYNKGKRVNLINKDI-RCKDDETHLYTLVIRPDNTYEVIDNSQVESGSL 179
DB 138 G-ASKRVHVLINYGKGNHLIKKINKVETDQLTHQYTLVISPNTYVNLVDNKEIQAGNL 196

RESULT 10
CRTC_EUGGR STANDARD; PRT; 401 AA.
ID CRTC_EUGGR
AC Q92NY3;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN PRECURSOR.
OS Euglena gracilis.
OS Eukaryote; Euglenozoa; Euglenida; Euglenales; Euglena.
OX NCBI_TaxID=3039;
RN [1]
RP SEQUENCE FROM N.A.
RT Navazio L., Balcan B., Martin W., Mariani P.;
RT "Evidence for conservation of a calcium homeostat component:
RT purification characterization and cloning of calreticulin from Euglen
RT gracilis.";
RL Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY)
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
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CC or send an email to licenset@isb-sib.ch).
CC -----
CC EMBL; Y09816; CAA70945.1;
CC InterPro; IPR001580; Calreticulin.
CC InterPro; IPR000886; ER_target.
CC Pfam; PF00262; calreticulin; 1.
CC PRINTS; PR00626; CALRETICULIN.
CC PRODOM; PD001866; Calreticulin; 1.
CC PROSITE; PS00014; ER_TARGET; 1.
CC PROSITE; PS00803; CALRETICULIN_1; 1.
CC PROSITE; PS00804; CALRETICULIN_2; 1.
CC PROSITE; PS00805; CALRETICULIN_REPEAT; FALSE_NEG.
CC Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 18
FT CHAIN 19 401
FT TAG POTENTIAL.
FT CALRETICULIN.

```

Query Match 54.7%; Score 531; DB 1; Length 416;
Best Local Similarity 55.9%; Pred. No. 1.6e-40;
Matches 100; Conservative 28; Mismatches 45; Indels 6; Gaps 3;

QY 4 VYKPEQFLDGDGWTSRWIESKHSD---FGKFVLSGKFGYDEKDKGLQTSODARFYAL 60
|:|:|:| 111 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11
Db 27 VFPEERF--EDGWEKRWKSEKMDSEAGWNYTSGKNGD-ANDKGIQTSYDFYAI 83
|:|:|:| 111 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11
QY 61 SASFEPSFKNGQTLVQFTVKHEQNDICGCGYVKKLPNSLDQDMHGDSEYNTMFGPDIC 120
|:|:|:| 111 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11
Db 84 SAEFPFSKNDKTLVQFVSVKHEQKLDGCGGYMKLLSGEVDQKFKFGDTPYSIMFGPDIC 143
|:|:|:| 111 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11
QY 121 GPCTCKVHVIFNYKGNVNLKINDIRCKDDETHLYTLVIRPDNTYEVKIDNSOVESGSL 179
|:|:|:| 111 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11
Db 144 GYSTKKVHAIFNYNDNHLIKKDVPCETDQLTHTVYTLIRPDATYSILINDQEKQTGSL 202
|:|:|:| 111 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11

RESULT 12
CRTC_RICCO
ID CRTC_RICCO STANDARD; PRT; 415 AA.
AC P93508;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN PRECURSOR.
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
OX NCBI_TaxID=3988;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97435975; PubMed=9290642;
RA Coughlan S.J., Hastings C., Winfrey R. Jr.;
RT "Cloning and characterization of the calreticulin gene from Ricinus communis L.";
RL Plant Mol. Biol. 34:897-911(1997).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC -!- LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U74631; AAB71420.1; -
CC EMBL; U74630; AAB71419.1; -
CC Mendel; 10452; Ricco.1166;10452
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER-target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 415 CALRETICULIN.
FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 412 415 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 415 AA; 47522 MW; DD5F452E76CC7F8C CRC64;

Query Match 54.3%; Score 527; DB 1; Length 415;
Best Local Similarity 55.3%; Pred. No. 3.6e-40;

Matches 99; Conservative 31; Mismatches 43; Indels 6; Gaps 3;

QY 4 VYKPEQFLDGDGWTSRWIESKHSD---FGKFVLSGKFGYDEKDKGLQTSODARFYAL 60
|:|:|:| 111 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11
Db 22 VFPEERF--EDGWEKRWKSKDKDENTAGENWNTSGKNGD-PNDKGIQTSYDFYAI 78
|:|:|:| 111 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11
QY 61 SASFEPSFKNGQTLVQFTVKHEQNDICGCGYVKKLPNSLDQDMHGDSEYNTMFGPDIC 120
|:|:|:| 111 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11
Db 79 SAEFPFSKNDKTLVQFVSVKHEQKLDGCGGYMKLLSSSTDQKFKFGDTPYSIMFGPDIC 138
|:|:|:| 111 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11
QY 121 GPCTCKVHVIFNYKGNVNLKINDIRCKDDETHLYTLVIRPDNTYEVKIDNSOVESGSL 179
|:|:|:| 111 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11
Db 139 GYSTKKVHAIFNYNDNHLIKKDVPCETDQLTHTVYTLIRPDATYSILINDQEKQTGSL 197
|:|:|:| 111 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11

RESULT 13
CRTC_PUAR
ID CRTC_PUAR STANDARD; PRT; 421 AA.
AC Q9XF98;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN PRECURSOR.
OS Prunus armeniaca (Apricot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Prunus.
OX NCBI_TaxID=36596;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. BERGERON; TISSUE=Mesocarp, and Endocarp;
RA Mbeugue-A-Mbeugue D., Fils-Lycaon B.R.;
RT "Molecular cloning and nucleotide sequence of a calreticulin from apricot (Prunus armeniaca cv. Bergeron).";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC -!- LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC
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CC
CC EMBL; AF134733; AAD32207.1; -
CC InterPro; IPR001580; Calreticulin.
CC InterPro; IPR000886; ER-target.
CC Pfam; PF00262; calreticulin; 1.
CC PRINTS; PR00626; CALRETICULIN.
CC ProDom; PD001866; Calreticulin; 1.
CC PROSITE; PS00014; ER_TARGET; 1.
CC PROSITE; PS00803; CALRETICULIN_1; 1.
CC PROSITE; PS00804; CALRETICULIN_2; 1.
CC PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 421 CALRETICULIN.
FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 418 421 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 421 AA; 48416 MW; 4F5F94CBAA6C6690 CRC64;

Query Match 54.3%; Score 527; DB 1; Length 421;
Best Local Similarity 55.3%; Pred. No. 3.7e-40;
Matches 99; Conservative 28; Mismatches 46; Indels 6; Gaps 3;

QY 4 VYKPEQFLDGDGWTSRWIESKHSD---FGKFVLSGKFGYDEKDKGLQTSODARFYAL 60
|:|:|:| 111 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11 |:|:|:| 11

Db 26 VFEERF--EDGWRKRVTSWKNDENLAGENWNTSGKMGD-PNDKGIQTSEDYRFVAI 82
 QY 61 SASPEFNSKGTLLVQVTVRHEQNDICGGGVYKLFPSNLSLQTDHMGDSSEYNMGPDIC 120
 Db 83 SAEPFNSKGTLLVQVTVRHEQNDICGGGVYKLFPSNLSLQTDHMGDSSEYNMGPDIC 142
 QY 121 GPGTKKHVIFNKGKVLINKDKDDETHLYTLVRPDPNTVEYKIDNSQVSGSL 179
 Db 143 GYSTKKVHAILNNTNNLKKDVPCEFDQLTHVTFIRDPATYSILIDNLEKOTGSL 201

RESULT 14

CRTC_ORYSA
 ID CRTC_ORYSA STANDARD; PRT; 424 AA.

AC Q9SLY8;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE CALRETICULIN PRECURSOR.
 OS Oryza sativa (Rice).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC Ehrhacoidae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Komatsu S., Li Z.;
 RT "Cloning the cDNA encoding a calcium-binding protein which involved in
 the regeneration of rice cultured suspension cells.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

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 CC or send an email to license@isb-sib.ch).

DR EMBL; AB021259; BAA88900.1;
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR000886; ER target.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR PRODOM; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER-TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 1.
 DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
 FT SIGNAL 1 29 POTENTIAL.
 FT CHAIN 30 424 CALRETICULIN.
 FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SITE 421 424 PREVENT SECRETION FROM ER (POTENTIAL).
 SQ SEQUENCE 424 AA; 47925 MW; 3172634F1580FC14 CRC64;

Query Match 54.3%; Score 527; DB 1; Length 424;

Best Local Similarity 55.9%; Pred. No. 3.7e-40;
 Matches 100; Conservative 31; Mismatches 42; Indels 6; Gaps 3;

QY 4 VYFKQFLDGGWTSRWIESKHSD---FGKPVLSGGKFYGDDEKDKGLQTSQDARFVAL 60
 Db 31 VYFQKFE--EDGWESRWYKSEKKKDNMAGENWNTSGKMGDPD-DKGIQTSEDYRFVAI 87
 QY 61 SASPEFNSKGTLLVQVTVRHEQNDICGGGVYKLFPSNLSLQTDHMGDSSEYNMGPDIC 120
 Db 88 SAEPFNSKGTLLVQVTVRHEQNDICGGGVYKLFPSNLSLQTDHMGDSSEYNMGPDIC 147

QY 121 GPGTKKHVIFNKGKVLINKDKDDETHLYTLVRPDPNTVEYKIDNSQVSGSL 179
 Db 148 GYSTKKVHTFTFKNDKNHLIKKDVPCETDQLSHVTLIHPDATYSILIDNVEKSGSI 206

RESULT 15

CRT2_BOVIN
 ID CRT2_BOVIN STANDARD; PRT; 421 AA.

AC P42918;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE CALRETICULIN, BRAIN ISOFORM 2 PRECURSOR (CRP55) (CALREGULIN) (HACBP).
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Brain;
 RX MEDLINE=93385184; PubMed=8373827;
 RA Liu N., Fine R.E., Johnson R.J.;
 RT "Comparison of cDNAs from bovine brain coding for two isoforms of
 calreticulin.";
 RL Biochim. Biophys. Acta 1202:70-76(1993).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

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 CC or send an email to license@isb-sib.ch).

DR EMBL; L13462; AAC37307.1;
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR000886; ER target.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR PRODOM; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER-TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 34 POTENTIAL.
 FT CHAIN 35 421 CALRETICULIN, BRAIN ISOFORM 2.
 FT DOMAIN 35 201 N-DOMAIN.
 FT DOMAIN 202 312 P-DOMAIN.
 FT DOMAIN 313 421 C-DOMAIN.
 FT DOMAIN 195 259 4 X APPROXIMATE REPEATS.
 FT REPEAT 195 206 1-1.
 FT REPEAT 214 225 1-2.
 FT REPEAT 231 242 1-3.
 FT REPEAT 248 259 1-4.
 FT DOMAIN 263 301 3 X APPROXIMATE REPEATS.
 FT REPEAT 263 273 2-1.
 FT REPEAT 277 287 2-2.
 FT REPEAT 291 301 2-3.
 FT DOMAIN 366 411 ASP/GLU/LYS-RICH.
 FT DISULFID 141 167 BY SIMILARITY.
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SITE 418 421 PREVENT SECRETION FROM ER.
 SQ SEQUENCE 421 AA; 48612 MW; 0257959F71528BC CRC64;

Query Match

53.8%; Score 522.5; DB 1; Length 421;

Best Local Similarity 55.6%; Pred. No. 9.4e-40;
Matches 109; Conservative 12; Mismatches 30; Indels 45; Gaps 4;

QY	1	EPAYVFKQFLDGDGWTSRWIESKHKSD-----FGKFVLSSGKFGYGDDE	44
Db	35	EETVVFSEQLT-----LDLKYKASKLSSIREALSMKVGIIENFCFSEISFLQESI	86
QY	45	KDKGLQTSQDARFYALSASFEPFSNKGQTLVQFTVKHEQNIDCGGGYVKLFPNSLDQTD	104
Db	87	KSHGRRT-----LVGCSPWGHE-----EQNIDCGGGYVNVFPAGLDQTD	125
QY	105	MHGDSEYNIMFGPDICGPGTKKVHVIFNYKGNVLINKDIRCKDDETHLYTLIVRPDNT	164
Db	126	MHGDSEYNIMFGPDICGPGTKKVHVIFNYKGNVLINKDIRCKDDETHLYTLIVRPNT	185
QY	165	YEVKIDNSQVESGSLE	180
Db	186	YEVKIDNSQVESGSLE	201

Search completed: January 9, 2002, 15:12:14
Job time: 656 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 9, 2002, 14:58:58 ; Search time 78.15 Seconds
(without alignments)
336.904 Million cell updates/sec

Title: US-09-828-000-3
Perfect score: 971
Sequence: 1 EPAYVYFKEQFLDGDGWSRW.....PDNTYEVKIDNSQVSGSLE 180

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 14627329 residues
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_17.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phase.*
 - 10: sp_plant.*
 - 11: sp_prodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	835	86.0	411	13	Q91710 xenopus lae
2	804	82.8	405	5	Q26268 alypsia cal
3	797	82.1	343	13	Q91711 xenopus lae
4	796	82.0	419	13	Q98984 rana rugosa
5	785	80.8	417	13	Q9PUC1 Q9pucl brachydanio
6	759	78.2	410	5	Q16893 amblyomma a
7	731	75.3	421	5	Q9U6S0 Q9u6s0 strongyloce
8	699	72.0	406	5	Q9U916 Q9u916 drosophila
9	681.5	70.2	403	5	O76961 O76961 necator ame
10	680	70.0	387	5	O97372 O97372 dirofilaria
11	673	69.3	375	5	O18478 O18478 litomoscoide
12	641	66.0	380	11	Q9D9Q6 Q9d9q6 mus musculus
13	539	55.5	412	10	Q40040 Q40040 hordeum vul
14	539	55.5	415	10	Q40041 Q40041 hordeum vul
15	536	55.2	421	10	Q43712 Q43712 zea mays (m
16	517	53.2	389	10	Q40567 Q40567 nicotiana t
17	514.5	53.0	427	10	Q9FV2 Q9fyv2 pinus taeda
18	507.5	52.3	396	5	O45034 O45034 schistosoma
19	477.5	49.2	350	5	Q26514 Q26514 schistosoma

20	464.5	47.8	240	10	Q9ST29 Q9st29 solanum mel
21	460	47.4	318	13	Q9PTX7 Q9ptx7 lampetra re
22	450	46.3	214	4	Q9UDG2 Q9udg2 homo sapien
23	448.5	46.2	403	5	Q9XYF8 Q9xyf8 trypanosoma
24	446.5	46.0	401	5	Q9U9N9 Q9u9n9 trypanosoma
25	409.5	42.2	291	5	Q9XIV1 Q9xivi leishmania
26	332	40.4	397	5	Q94592 Q94592 leishmania
27	373	38.4	321	13	Q9U5G0 Q9u5g0 eptatretus
28	347	35.7	422	10	O22502 O22502 brassiga na
29	329.5	33.9	321	10	O41799 O41799 zea mays (m
30	302.5	31.2	101	10	Q40751 Q40751 parthenium
31	289.5	29.8	582	3	Q9HFC6 Q9hfc6 yarrowia li
32	270	27.8	578	11	Q9D2K5 Q9d2k5 mus musculu
33	264.5	27.2	559	5	Q9NG26 Q9ng26 tritrichomo
34	263.5	27.1	581	5	Q9BLH3 Q9blh3 halocynthia
35	262	27.0	622	13	Q98985 Q98985 rana rugosa
36	251	25.8	70	10	Q9SXW3 Q9sxn3 lithospernu
37	248	25.5	582	5	Q04702 Q04702 schistosoma
38	240	24.7	583	5	Q9VXF6 Q9vxf6 drosophila
39	238.5	24.6	582	5	O76214 O76214 schistosoma
40	238.5	24.6	582	5	Q9TVF3 Q9tvf3 schistosoma
41	231.5	23.8	272	4	Q16094 Q16094 homo sapien
42	224	23.1	543	5	Q9VYP4 Q9vyp4 drosophila
43	224	23.1	556	5	Q9I7S9 Q9i7s9 drosophila
44	221.5	22.8	605	5	O02393 O02393 drosophila
45	207	21.3	545	5	Q9VAL7 Q9val7 drosophila

ALIGNMENTS

RESULT 1	
Q91710	
ID	Q91710 PRELIMINARY; PRT; 411 AA.
AC	Q91710;
DT	01-JAN-1998 (TREMBLrel. 05, Created)
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE	CALRETICULIN PRECURSOR (FRAGMENT).
OS	Xenopus laevis (African clawed frog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC	Xenopodinae; Xenopus.
OX	NCBI_TaxID=8355;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=BRAIN;
RX	MEDLINE=93074997; PubMed=1445218;
RA	Treves S., Zorzato F., Pozzan T.;
RT	"Identification of calreticulin isoforms in the central nervous
RT	system.";
RL	Biochem. J. 287:579-581(1992).
DR	EMBL; X67597; CAA47866.1; .
DR	InterPro; IPR000886; ER_target.
DR	InterPro; IPR001580; Calreticulin.
DR	Pfam; PF00262; calreticulin; 1.
DR	PRINTS; PR00626; CALRETICULIN.
DR	ProDom; PD001866; Calreticulin; 1.
DR	PROSITE; PS00803; CALRETICULIN_1; 1.
DR	PROSITE; PS00804; CALRETICULIN_2; 1.
DR	PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR	PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW	Signal.
FT	NON_TER 1 1
FT	SIGNAL <1 12 POTENTIAL.
FT	CHAIN 13 411 CALRETICULIN.
SQ	SEQUENCE 411 AA; 48344 MW; 891DA66E0EBEFA CRC64;

Query Match 86.0%; Score 835; DB 13; Length 411;
Best Local Similarity 83.9%; Pred. No. 2.7e-71;
Matches 151; Conservative 15; Mismatches 14; Indels 0; Gaps 0;

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QY 1 EPAYVFKQFLDGDGWTSMWIESKHKSDFKFLVLSGKFGYDEKDKGLQTSQDARFYAL 60
DB 13 EPAYVFKKEFTDGDGWTQWVESKHKTGYGKFLSAGKFGYDSEKDKGLQTSQDARFYAM 72
QY 61 SASFPFSSKNGTGLVQVFTVKHEQNIDCGGKFLPNSLDQTDHMGDSYNIIMFGPDIC 120
DB 73 SRFDSFSSKNGTGLVQVFTVKHEQNIDCGGKFLPNSLDQTDHMGDSYNIIMFGPDIC 132
QY 121 GPCTKKVHVIFNYKGNVLINKDIRCKDDFTHLTYTLIVRPDNTYEVKIDNSQVSGSLE 180
DB 133 GPPTKKVHVIFQYKKNLQINKDIRCKDDFTHLTYTLIVRPDNTYEVKIDNSQVSGSLE 192
RESULT 2
ID Q26268 PRELIMINARY; PRT; 405 AA.
AC Q26268;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CALRETICULIN.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidia;
OC Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93098937; PubMed=1463604;
RA Kennedy T.E., Kuhl D., Barzilai A., Sweatt J.D., Kandel E.R.;
RT "Long-term sensitization training in Aplysia leads to an increase in
RT calreticulin, a major presynaptic calcium-binding protein.";
RL Neuron 9:1013-1024(1992).
DR EMBL: S51239; A824569.1; -;
DR InterPro; IPR000886; ER-target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS0014; ER-TARGET; UNKNOWN_1.
SQ SEQUENCE 405 AA; 46738 MW; 14CAA201840DID69 CRC64;
Query Match 82.8%; Score 804; DB 5; Length 405;
Best Local Similarity 79.4%; Pred. No. 2,3e-68;
Matches 143; Conservative 18; Mismatches 17; Indels 2; Gaps 1;
QY 1 EPAYVFKQFLDGDGWTSMWIESKHKSDFKFLVLSGKFGYDEKDKGLQTSQDARFYAL 60
DB 16 DTVVFKKEF--GDDWAERWVESKHKSGLGKFLTAGKFGYDAEKDKGLQTSQDARFYGL 73
QY 61 SASFPFSSKNGTGLVQVFTVKHEQNIDCGGKFLPNSLDQTDHMGDSYNIIMFGPDIC 120
DB 74 SARFDSFSSKNGTGLVQVFTVKHEQNIDCGGKFLPNSLDQTDHMGDSYNIIMFGPDIC 133
QY 121 GPCTKKVHVIFNYKGNVLINKDIRCKDDFTHLTYTLIVRPDNTYEVKIDNSQVSGSLE 180
DB 134 GPCTKKVHVIFNYKGNLVLKDKDIRCKDDFTHLTYTLIVRPDNTYEVKIDNSQVSGSLE 193
RESULT 3
ID Q91711 PRELIMINARY; PRT; 343 AA.
AC Q91711;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CALRETICULIN (FRAGMENT).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
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OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=93074997; PubMed=1445218;
RA Treves S., Zorzato F., Pozzan T.;
RT "Identification of calreticulin isoforms in the central nervous
RT system.";
RL Biochem. J. 287:579-581(1992).
DR EMBL; X67598; CAA47867.1; -;
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
FT NON_TER 1
FT NON_TER 343
SQ SEQUENCE 343 AA; 40105 MW; 3E7DDAFA33B91DE1 CRC64;
Query Match 82.1%; Score 797; DB 13; Length 343;
Best Local Similarity 85.2%; Pred. No. 8,7e-68;
Matches 144; Conservative 12; Mismatches 13; Indels 0; Gaps 0;
QY 12 DGDGWTSMWIESKHKSDFKFLVLSGKFGYDEKDKGLQTSQDARFYALSASFPFSSKNG 71
DB 1 DGDGWTQWVESKHKSDFKFLSAGKFGYDSEKDKGLQTSQDARFYAMSRFSPSKND 60
QY 72 QTLVQVFTVKHEQNIDCGGKFLPNSLDQTDHMGDSYNIIMFGPDICGCTKKVHVIF 131
DB 61 QTLVQVFTVKHEQNIDCGGKFLPNSLDQTDHMGDSYNIIMFGPDICGCTKKVHVIF 120
QY 132 NYKGNVLINKDIRCKDDFTHLTYTLIVRPDNTYEVKIDNSQVSGSLE 180
DB 121 QYKKNLQINKDIRCKDDFTHLTYTLIVRPDNTYEVKIDNSQVSGSLE 169
RESULT 4
Q98984 PRELIMINARY; PRT; 419 AA.
ID Q98984;
AC Q98984;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CALRETICULIN.
OS Rana rugosa (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96234004; PubMed=8654561;
RA Yamamoto S., Nakamura M.;
RT "Calnexin: its molecular cloning and expression in the liver of the
RT frog, Rana rugosa.";
RL FEBS Lett. 387:27-32(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Yamamoto S.;
RT "Strong expression of the calreticulin gene in the liver of Rana
RT rugosa Tadpoles.";
RL J. Exp. Zool. 0:0-0(1996).
DR EMBL; D78589; BAA11425.1; -;
DR InterPro; IPR000886; ER-target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
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DR EMBL; X89813; CAA61939.1; -
DR Mendel; 11228; Zeama;1166;11228.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Signal; Calcium-binding.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 421 CALRETICULIN.
SQ SEQUENCE 421 AA; 48012 MW; 5AAE02B77ED3126D CRC64;

Query Match 55.2%; Score 536; DB 10; Length 421;
Best Local Similarity 56.4%; Pred. NO. 6.7e-43;
Matches 101; Conservative 31; Mismatches 41; Indels 6; Gaps 3;

QY 4 VYKKEQFLDGDGWTGRWIESKHKSD--FGKTVLSSGKFGYGDDEKDKGLQTSQDARFYAL 60
Db 27 VFFQEKF--EDGWESRWKSEWKKDENWAGWNHTSGKWNDAE--DKGIQTSEDYRFYAI 83

QY 61 SASFEPFNKGQTLVYVQFTVKHEQNIIDCGGYVKLFNPSLDQTDHMGDSEYNIMFGPDIC 120
Db 84 SAEYEPFSNKDKTLVLQFSVKHEQKLDCCGGYVKLLGGDVQDKFEGGDTSYSIMFGPDIC 143

QY 121 GPGTKKHVIFNPKKNVLINKDKCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSSGL 179
Db 144 GYSTRKKVHTILT KDGNHLIRKDKVPCETDQLTHVYTLIIRPDATYSILIDNEEKQTGSI 202
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Search completed: January 9, 2002, 15:03:27
Job time: 269 sec

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